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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 21:13:15 ; Search time 2021.2 Seconds
(without alignments)
813.555 Million cell updates/sec

Title: US-10-766-691-9
Perfect score: 1041
Sequence: 1 atggaagtgatgaaaaatt.....aggactctccgctcaaaagt 1041

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9168763 seqs, 789795712 residues

Total number of hits satisfying chosen parameters: 18337526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
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10: /cgn2_6/ptodata/1/pna/US13_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	729.6	70.1	1618	2 PCT-US05-03526-3
2	572	54.9	1400	10 US-11-060-756-23
3	572	54.9	1400	10 US-11-060-756-4295
4	567.4	54.5	600	10 US-11-060-756-22
5	567.4	54.5	600	10 US-11-060-756-4294
6	368	35.4	600	10 US-11-060-756-1500
7	368	35.4	600	10 US-11-060-756-1501
8	368	35.4	600	10 US-11-060-756-5772
9	368	35.4	600	10 US-11-060-756-5773
10	343.8	33.0	1175	10 US-11-060-756-3884
11	343.8	33.0	1175	10 US-11-060-756-3885
12	343.8	33.0	1175	10 US-11-060-756-8156
13	343.8	33.0	1175	10 US-11-060-756-8157
14	285.6	27.4	600	10 US-11-060-756-37
15	285.6	27.4	600	10 US-11-060-756-38
16	285.6	27.4	600	10 US-11-060-756-4309
17	285.6	27.4	600	10 US-11-060-756-4310
18	241.2	23.2	1993	2 PCT-US05-03526-1
19	202.6	19.5	1513	2 PCT-US05-03526-2
20	177.4	17.0	1158	8 US-10-450-763-6133
21	177.2	17.0	3399	2 PCT-US05-03526-4

22	176.2	16.9	1400	10	US-11-060-756-523	Sequence 523, App
23	176.2	16.9	1400	10	US-11-060-756-4795	Sequence 4795, App
24	153.4	14.7	1323	10	US-11-060-756-373	Sequence 373, App
25	153.4	14.7	1323	10	US-11-060-756-374	Sequence 374, App
26	153.4	14.7	1323	10	US-11-060-756-4645	Sequence 4645, App
27	153.4	14.7	1323	10	US-11-060-756-4646	Sequence 4646, App
28	151	14.5	1522	9	US-11-085-606-1008	Sequence 1008, App
29	151	14.5	2012	9	US-11-085-606-1012	Sequence 1012, App
30	146.2	14.0	1184	9	US-11-099-266-92	Sequence 92, Appl
31	146.2	14.0	1184	10	US-11-036-196-1727	Sequence 1727, App
32	142.6	13.7	600	10	US-11-060-756-3309	Sequence 3309, App
33	142.6	13.7	600	10	US-11-060-756-7581	Sequence 7581, App
34	134.8	12.9	1161	1	PCT-US05-10257-245	Sequence 245, App
35	134.8	12.9	1825	7	US-10-122-851-313	Sequence 313, App
36	133.2	12.8	1089	1	PCT-US05-10257-244	Sequence 244, App
37	116.2	11.2	1738	8	US-10-450-763-5885	Sequence 5885, App
38	115	11.0	1400	10	US-11-060-756-241	Sequence 241, App
39	115	11.0	1400	10	US-11-060-756-242	Sequence 242, App
40	115	11.0	1400	10	US-11-060-756-4513	Sequence 4513, App
41	115	11.0	1400	10	US-11-060-756-4514	Sequence 4514, App
42	112	10.8	1311	7	US-10-489-448-837	Sequence 837, App
43	111.6	10.7	909	7	US-10-932-182A-81516	Sequence 81516, A
44	111.2	10.7	837	2	PCT-US05-07748-92	Sequence 92, Appl
45	111	10.7	1310	7	US-10-525-647-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
PCT-US05-03526-3
; Sequence 3, Application PC/TUS0503526
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: WMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
; FILE REFERENCE: EX05-003C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03526
; PRIOR FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,835
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1618
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US05-03526-3

Query Match 70.1%; Score 729.6; DB 2; Length 1618;
Best Local Similarity 84.6%; Pred. No. 6.2e-143;
Matches 893; Conservative 0; Mismatches 49; Indels 114; Gaps 2;

QY	4	GAAAGTATGAAAAATTAGCTAGCACTGGAGAGGGTCTTATGGGTTGTATTCAAATGC	63
DB	496	GACCCGTATGAAAAATTAGCTAGCACTGGAGAGGGTCTTATGGGTTGTATTCAAATGC	555
QY	64	AGAAACAAACCTCTGGCAAGTAGTCTCTTAAAAAATTGTGGAATCTGAAGATCAT	123
DB	556	AGAAACAAACCTCTGGCAAGTAGTCTCTTAAAAAATTGTGGAATCTGAAGATCAT	615
QY	124	CCTGTTGTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACATCCA	183
DB	616	CCTGTTGTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACATCCA	675
QY	184	AATCTTGTGAACCTCATCGAGGTCTTCAAGAGAAAGAAATGCAATTTAGTTTGA	243
DB	676	AATCTTGTGAACCTCATCGAGGTCTTCAAGAGAAAGAAATGCAATTTAGTTTGA	735
QY	244	TACTGTGATCATACACATTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGATGA	303
DB	736	TACTGTGATCATACACATTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGATGA	795
QY	304	GTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTGATATACATA--	361

Db 796 AGCATCGTGGCCCTCTCAGAGAGTGTGCTCATCGTTCAGGTTAGCTCCGAAAAATAAT 855
Qy 362 -----ACTGATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACT 405
Db 856 CAAATAATATGATCTTACAGTGTATTACAGAGATATAAAACCTGAAATATTTCTAAATACT 915
Qy 406 AAGCAAGGAATAATCAAGATTTGACCTCGGGTTTCACAAATTCGATTCAGAGAGAT 465
Db 916 AAGCAAGGAATAATCAAGATTTGACCTCGGGTTTCACAAATTCGATTCAGAGAGAT 975
Qy 466 GCCTACACCGATATTAGTACAGATGATACCGAGCTCCTGAACTTTCTTTGGGAGAT 525
Db 976 GCCTACACCGATATTAGTACAGATGATACCGAGCTCCTGAACTTTCTTTGGGAGAT 1035
Qy 526 ACTCAGTATGGTCTTCAGTCGATATATGGGCTATATGGTGTGTTTTCAGAGCTCCTG 585
Db 1036 ACTCAGTATGGTCTTCAGTCGATATATGGGCTATATGGTGTGTTTTCAGAGCTCCTG 1095
Qy 586 ACAGGCCAGCACTGCGCTGGAATATCAGATGTGGACCACTTTATCTGATAATCAGA 645
Db 1096 ACAGGCCAGCACTGCGCTGGAATATCAGATGTGGACCACTTTATCTGATAATCAGA 1155
Qy 646 ACCTTAGTAGAGACGGGTTTCGCCATGTTCACCAAGCTGCTCTCGAACTCTTGACGTCA 705
Db 1156 ACCT----- 1160
Qy 706 AGTGATCCACCTGCGGTAGCTCTCAAGTGTCTGGAATTCAGAAATAATATCCCAAGA 765
Db 1161 -----AGGAAATAATATCCCAAGA 1179
Qy 766 CATCAATCAATCTTAAAGTAAAGGTTTTCATGGCATCAGTATACCTGAGCCAGAA 825
Db 1180 CATCAATCAATCTTAAAGTAAAGGTTTTCATGGCATCAGTATACCTGAGCCAGAA 1239
Qy 826 GACATGAAACTCTTGAGGAAAGTTCTCAGATGTTCATCGTGGCTCTGAACTTCATG 885
Db 1240 GACATGAAACTCTTGAGGAAAGTTCTCAGATGTTCATCGTGGCTCTGAACTTCATG 1299
Qy 886 AAGGGGTCTGGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCGGAGAC 945
Db 1300 AAGGGGTCTGGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCGGAGAC 1359
Qy 946 TCCTACTTTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGTAATGAAGGAAGA 1005
Db 1360 TCCTACTTTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGTAATGAAGGAAGA 1419
Qy 1006 AACAGAAGACGCCAACAGGTACTTCCGCTCAAAAGT 1041
Db 1420 AACAGAAGACGCCAACAGGTACTTCCGCTCAAAAGT 1455

RESULT 2
US-11-060-756-23
; Sequence 23, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match. 54.9%; Score 572; DB 10; Length 1400;
Best Local Similarity 100.0%; Pred. No. 3.9e-110;

Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 454 ATTCAGAGGAGATCCCTACACCGATTATGTAGCTACAGATGGTACCGAGCTCCTGAACCTT 513
Db 478 ATTCAGAGGAGATCCCTACACCGATTATGTAGCTACAGATGGTACCGAGCTCCTGAACCTT 537
Qy 514 CTCTGTGGGAGATACTCAGTATGTTCTTTCAGTCGATATATGGGCTATATGGTGTGTTTTT 573
Db 538 CTCTGTGGGAGATACTCAGTATGTTCTTTCAGTCGATATATGGGCTATATGGTGTGTTTTT 597
Qy 574 GCAGAGCTCCTGACAGGCCAGCCACTGTGGCTCGGAAATCAGATGTGGACCACTTTAT 633
Db 598 GCAGAGCTCCTGACAGGCCAGCCACTGTGGCTCGGAAATCAGATGTGGACCACTTTAT 657
Qy 634 CTGATATCAGACACTAGTAGAGACGGGTTTCGCCATGTTCACCAAGCTGCTCTCGAA 693
Db 658 CTGATATCAGACACTAGTAGAGACGGGTTTCGCCATGTTCACCAAGCTGCTCTCGAA 717
Qy 694 CTCTTGACGCTCAAGTGATCCACCTGCGGTAGCTCTCAAAGTCTCGAAATTCAGGAAAA 753
Db 718 CTCTTGACGCTCAAGTGATCCACCTGCGGTAGCTCTCAAAGTCTCGAAATTCAGGAAAA 777
Qy 754 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAAGGTTTTCATGGCATCAGTATA 813
Db 778 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAAGGTTTTCATGGCATCAGTATA 837
Qy 814 CCTGAGCCGACAGACATGGAACCTCTTGAGGAAAAAGTTCTCAGATGTTCATCTGTGGCT 873
Db 838 CCTGAGCCGACAGACATGGAACCTCTTGAGGAAAAAGTTCTCAGATGTTCATCTGTGGCT 897
Qy 874 CTGAACTTCATGAAGGGGTCTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCAA 933
Db 898 CTGAACTTCATGAAGGGGTCTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCAA 957
Qy 934 CTCTGTGAGAGCTCTTACTTTTGAATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGT 993
Db 958 CTCTGTGAGAGCTCTTACTTTTGAATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGT 1017
Qy 994 AATGAGGAGAAACAGAGACGCCCAACAGGT 1025
Db 1018 AATGAGGAGAAACAGAGACGCCCAACAGGT 1049
RESULT 3
US-11-060-756-4295
; Sequence 4295, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4295
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-4295
Query Match 54.9%; Score 572; DB 10; Length 1400;
Best Local Similarity 100.0%; Pred. No. 3.9e-110;
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 454 ATTCAGAGGAGATCCCTACACCGATTATGTAGCTACAGATGGTACCGAGCTCCTGAACCTT 513
Db 478 ATTCAGAGGAGATCCCTACACCGATTATGTAGCTACAGATGGTACCGAGCTCCTGAACCTT 537
Qy 514 CTCTGTGGGAGATACTCAGTATGTTCTTTCAGTCGATATATGGGCTATATGGTGTGTTTTT 573
Db 538 CTCTGTGGGAGATACTCAGTATGTTCTTTCAGTCGATATATGGGCTATATGGTGTGTTTTT 597

Qy 574 GCAGAGCTCCTGACAGCGCCAGCCACTGTGGCCTCGAAATTCAGATGTGGACCAACTTTAT 633
 Db 598 GCAGAGCTCCTGACAGCGCCAGCCACTGTGGCCTCGAAATTCAGATGTGGACCAACTTTAT 657
 Qy 634 CTGATAATCAGAACACTAGTAGACAGCGGGTTTCGCCATGTGTGACCAAGGCTGGTCTCGAA 693
 Db 658 CTGATAATCAGAACACTAGTAGACAGCGGGTTTCGCCATGTGTGACCAAGGCTGGTCTCGAA 717
 Qy 694 CTCCTGACGTCAGTATCCACCTGCGGTAGCCTCTCAAAAGTGTGGAATTTACAGAGAAA 753
 Db 718 CTCCTGACGTCAGTATCCACCTGCGGTAGCCTCTCAAAAGTGTGGAATTTACAGAGAAA 777
 Qy 754 TTAATCCAGACATCAATCAATCTTTAAAGTAACCGGGTTTTCATGGCATCAGTATA 813
 Db 778 TTAATCCAGACATCAATCAATCTTTAAAGTAACCGGGTTTTCATGGCATCAGTATA 837
 Qy 814 CCTGAGCCAGAGACATGGAACCTCTTGAGGAAAGTCTCAGATGTTCATCCTGTGGCT 873
 Db 838 CCTGAGCCAGAGACATGGAACCTCTTGAGGAAAGTCTCAGATGTTCATCCTGTGGCT 897
 Qy 874 CTGAATCTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAA 933
 Db 898 CTGAATCTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAA 957
 Qy 934 CTCCTGAGAGCTCCTACTTTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACGCT 993
 Db 958 CTCCTGAGAGCTCCTACTTTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACGCT 1017
 Qy 994 AATGAAGGAGAAACAGAGACGCGCAACAGT 1025
 Db 1018 AATGAAGGAGAAACAGAGACGCGCAACAGT 1049

RESULT 4
 US-11-060-756-22
 ; Sequence 22, Application US/11060756
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; TITLE OF INVENTION: Target Genes
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 22
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-060-756-22

Query Match 54.5%; Score 567.4; DB 10; Length 600;
 Best Local Similarity 98.4%; Pred. No. 3.2e-109;
 Matches 562; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 Qy 471 CACCGATTATGTAGCTACGAGATGTTACCGAGCTCTCGAACTTCTGTGGAGATCTCA 530
 Db 1 CACCGATTATGTAGCTACGAGATGTTACCGAGCTCTCGAACTTCTGTGGAGATCTCA 60
 Qy 531 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGG 590
 Db 61 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGG 120
 Qy 591 CCAGCCACTGTGGCTCGAAATCAGATGTGGAACAACTTTATCTGATAATCAGAACACT 650
 Db 121 CCAGCCACTGTGGCTCGAAATCAGATGTGGAACAACTTTATCTGATAATCAGAACACT 180
 Qy 651 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTTGTGAGCTCAAGTGA 710
 Db 181 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTTGTGAGCTCAAGTGA 240

Qy 711 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAATTAATCCAGACATCA 770
 Db 241 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAATTAATCCAGACATCA 300
 Qy 771 ATCAATCTTTAAAGTAACCGGGTTTTCATGGCATCAGTATACCTCAGCCAGAGACAT 830
 Db 301 ATCAATCTTTAAAGTAACCGGGTTTTCATGGCATCAGTATACCTCAGCCAGAGACAT 360
 Qy 831 GGAAACTCTTTGAGGAAAGTCTCAGATGTTCATCTGTGGCTGAACTTTCATGAAGGG 890
 Db 361 GGAAACTCTTTGAGGAAAGTCTCAGATGTTCATCTGTGGCTGAACTTTCATGAAGGG 420
 Qy 891 GTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCCAACTCTCTGAGAGCTCTTA 950
 Db 421 GTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCCAACTCTCTGAGAGCTCTTA 480
 Qy 951 CTTTGATCTTTTCAAGAGGCCCAAAATTAAGAAAGACAGTAAATGAAGAAAGACAG 1010
 Db 481 CTTTGATCTTTTCAAGAGGCCCAAAATTAAGAAAGACAGTAAATGAAGAAAGACAG 540
 Qy 1011 AAGACGCCAACAGGTACTTCCGCTCAAAAGT 1041
 Db 541 AAGACGCCAACAGGTACTCCKMSGCTCRWRWT 571

RESULT 5
 US-11-060-756-4294
 ; Sequence 4294, Application US/11060756
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; TITLE OF INVENTION: Target Genes
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4294
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-060-756-4294

Query Match 54.5%; Score 567.4; DB 10; Length 600;
 Best Local Similarity 98.4%; Pred. No. 3.2e-109;
 Matches 562; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 Qy 471 CACCGATTATGTAGCTACGAGATGTTACCGAGCTCTCGAACTTCTGTGGAGATCTCA 530
 Db 1 CACCGATTATGTAGCTACGAGATGTTACCGAGCTCTCGAACTTCTGTGGAGATCTCA 60
 Qy 531 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGG 590
 Db 61 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGG 120
 Qy 591 CCAGCCACTGTGGCTCGAAATCAGATGTGGAACAACTTTATCTGATAATCAGAACACT 650
 Db 121 CCAGCCACTGTGGCTCGAAATCAGATGTGGAACAACTTTATCTGATAATCAGAACACT 180
 Qy 651 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTTGTGAGCTCAAGTGA 710
 Db 181 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTTGTGAGCTCAAGTGA 240
 Qy 711 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAATTAATCCAGACATCA 770
 Db 241 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAATTAATCCAGACATCA 300
 Qy 771 ATCAATCTTTAAAGTAACCGGGTTTTCATGGCATCAGTATACCTCAGCCAGAGACAT 830
 Db 301 ATCAATCTTTAAAGTAACCGGGTTTTCATGGCATCAGTATACCTCAGCCAGAGACAT 360
 Qy 831 GGAAACTCTTTGAGGAAAGTCTCAGATGTTCATCTGTGGCTGAACTTTCATGAAGGG 890

:	NUMBER OF SEQ ID NOS:	303284			
:	SOFTWARE:	Patentin version 3.2			
:	SEQ ID NO	5773			
:	LENGTH:	600			
:	TYPE:	DNA			
:	ORGANISM:	Homo sapiens			
:	US-11-060-756-5773				
Query Match		35.4%;	Score 368;	DB 10;	Length 600;
Best Local Similarity		81.9%;	Pred. No. 1e-67;		
Matches 480;		Conservative 0;	Mismatches 10;	Indels 96;	Gaps 1;
Qy	438	GTTTGGCAAAATCTTGATTCCAGAGAGATGCCCTACACCGAATATGTAGCTACGAGATGGTA	497		
Db	9	GATTGTGCATTTTTCAGTTTCAGGAGATGCCCTACACCGAATATGTAGCTACGAGATGGTA	68		
Qy	498	CCGAGCTCCTGGAACCTTCTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATGGC	557		
Db	69	CCGAGCTCCTGGAACCTTCTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATGGC	128		
Qy	558	TATTGGTTGTGTTTTTTCGAGAGCTCCTGCAGAGCCAGCCACTGTGGCCTGGAAAAATCAGA	617		
Db	129	TATTGGTTGTGTTTTTTCGAGAGCTCCTGCAGAGCCAGCCACTGTGGCCTGGAAAAATCAGA	188		
Qy	618	TGTGGACCAACTTTATCTGATTAATCAGAACACTAGTAGAGACGGGTTTCGCCATGTTGA	677		
Db	189	TGTGGACCAACTTTATCTGATTAATCAGAACACT	221		
Qy	678	CCAGGCTGGTCTCGAACTCTTTGACGTCAAGTGATCCACCTGCCGTAGCCTCTCAAAGTGC	737		
Db	222		221		
Qy	738	TGGAATTACAGGAAAATTAATCCAGACATCAATCAATCTTTAAAAAGTAACGGGTTTTT	797		
Db	222	-----AGGAAAATTAATCCAGACATCAATCAATCTTTAAAAAGTAACGGGTTTTT	272		
Qy	798	CCATGGCATCAGTATACCTGAGCCAGAGACATCGAAACTCTTGAGGAAAAGTTCTCAGA	857		
Db	273	CCATGGCATCAGTATACCTGAGCCAGAGACATCGAAACTCTTGAGGAAAAGTTCTCAGA	332		
Qy	858	TGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGCAG	917		
Db	333	TGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGCAG	392		
Qy	918	ATTAACTGTTCCTCAACTCTCTGGAGAGCTCCTACTTTTGATTCTTTTCAAGAGGCCCAAT	977		
Db	393	ATTAACTGTTCCTCAACTCTCTGGAGAGCTCCTACTTTTGATTCTTTTCAAGAGGCCCAAT	452		
Qy	978	TAAAGAAAAGCAGTAAATGAAGGAGAAAACAGAAAGCGCAACAG	1023		
Db	453	TAAAGAAAAGCAGTAAATGAAGGAGAAAACAGAAAGCGCAACAG	498		
RESULT 10					
US-11-060-756-3884					
; Sequence 3884, Application US/11060756					
; GENERAL INFORMATION:					
; APPLICANT: Wyeth					
; APPLICANT: Mounts, William Martin					
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles					
; TITLE OF INVENTION: Target Genes					
; FILE REFERENCE: AM101083 (031896-042000)					
; CURRENT APPLICATION NUMBER: US/11/060,756					
; CURRENT FILING DATE: 2005-02-18					
; NUMBER OF SEQ ID NOS: 303284					
; SOFTWARE: Patentin version 3.2					
; SEQ ID NO 3884					
; LENGTH: 1175					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
US-11-060-756-3884					
Query Match		33.0%;	Score 343.8;	DB 10;	Length 1175;

Best Local Similarity 71.2%; Pred. No. 1.2e-62;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

QY 1 ATGGAAGATGAAAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 60
Db |||||
QY 32 ATGGAAGATGAAAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 91
Db |||||
QY 61 TGCAGAAACAAACCTCTGAGCAAGTAGTAGCTGTTTAAAAAATTTGCGAATCTGAAGT 120
Db |||||
QY 92 TGTAGAAACAGGGACACGGGTGAGATTGTGGCCATCAAGAGTTCTGGAATCAGAAGAT 151
Db |||||
QY 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAAGCAATTAACACAT 180
Db |||||
QY 152 GACCCCTGTATAGAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 211
Db |||||
QY 181 CCAAACTCTGTAACCTCTGAGGTGTTTCAAGAGAAATAGCTATGTTGAAAGCAATTAACACAT 240
Db |||||
QY 212 CCAAACTCTGTAACCTCTGAGGTGTTTCAAGAGAAATAGCTATGTTGAAAGCAATTAACACAT 271
Db |||||
QY 241 GAATATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 300
Db |||||
QY 272 GAATATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 331
Db |||||
QY 301 GAGTATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 360
Db |||||
QY 332 CATCTGCTGATCAAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 420
Db |||||
QY 361 AACTGTATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 451
Db |||||
QY 421 AAGATTTGATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 477
Db |||||
QY 452 AAGCTTTGATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 511
Db |||||
QY 478 TATGTAGCTACAGATGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 537
Db |||||
QY 512 TACGTGGCTACAGATGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 571
Db |||||
QY 538 TCTTACGTGATATAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 597
Db |||||
QY 572 CCCCCGGTGGATGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 631
Db |||||
QY 598 CTGTGGCTGGAATATAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 656
Db |||||
QY 632 CTGTGGCTGGAATATAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 690
Db |||||

RESULT 11
US-11-060-756-3885
; Sequence 3885, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3885
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-3885

Query Match 33.0%; Score 343.8; DB 10; Length 1175;
Best Local Similarity 71.2%; Pred. No. 1.2e-62;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

QY 1 ATGGAAGATGAAAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 60
Db |||||
QY 32 ATGGAAGATGAAAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 91
Db |||||
QY 61 TGCAGAAACAAACCTCTGAGCAAGTAGTAGCTGTTTAAAAAATTTGCGAATCTGAAGT 120
Db |||||
QY 92 TGTAGAAACAGGGACACGGGTGAGATTGTGGCCATCAAGAGTTCTGGAATCAGAAGAT 151
Db |||||
QY 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAAGCAATTAACACAT 180
Db |||||
QY 152 GACCCCTGTATAGAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 211
Db |||||
QY 181 CCAAACTCTGTAACCTCTGAGGTGTTTCAAGAGAAATAGCTATGTTGAAAGCAATTAACACAT 240
Db |||||
QY 212 CCAAACTCTGTAACCTCTGAGGTGTTTCAAGAGAAATAGCTATGTTGAAAGCAATTAACACAT 271
Db |||||
QY 241 GAATATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 300
Db |||||
QY 272 GAATATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 331
Db |||||
QY 301 GAGTATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 360
Db |||||
QY 332 CATCTGCTGATCAAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 420
Db |||||
QY 361 AACTGTATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 451
Db |||||
QY 421 AAGATTTGATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 477
Db |||||
QY 452 AAGCTTTGATCTGTGATCATACACTTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 511
Db |||||
QY 478 TATGTAGCTACAGATGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 537
Db |||||
QY 512 TACGTGGCTACAGATGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 571
Db |||||
QY 538 TCTTACGTGATATAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 597
Db |||||
QY 572 CCCCCGGTGGATGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 631
Db |||||
QY 598 CTGTGGCTGGAATATAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 656
Db |||||
QY 632 CTGTGGCTGGAATATAGCTGTTTAAATGAGCTGGAGAAATAGCTATGTTGAAAGCAATTAACACAT 690
Db |||||

RESULT 12
US-11-060-756-8156
; Sequence 8156, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8156
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-8156

Query Match 33.0%; Score 343.8; DB 10; Length 1175;
Best Local Similarity 71.2%; Pred. No. 1.2e-62;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

QY 1 ATGGAAGATGAAAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 60
Db |||||
QY 32 ATGGAAGATGAAAAATAGCTAAGCTGGAGAGGGTCTTATCGGGTGTGATTTCAAA 91
Db |||||
QY 61 TGCAGAAACAAACCTCTGAGCAAGTAGTAGCTGTTTAAAAAATTTGCGAATCTGAAGT 120
Db |||||
QY 92 TGTAGAAACAGGGACACGGGTGAGATTGTGGCCATCAAGAGTTCTGGAATCAGAAGAT 151
Db |||||

Db 289 AAGAAAAGCACGTATGAGGAGGAGAAACAGAGACGCCAACAGRWWCWDMBGYTSVCWV 348

RESULT 15
US-11-060-756-38
; Sequence 38, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-38

Query Match 27.4%; Score 285.6; DB 10; Length 600;
Best Local Similarity 94.3%; Pred. No. 1.4e-50;
Matches 283; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
QY 740 GAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTC 799
Db 49 GAACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTC 108
QY 800 ATGGCATCAGTATACCTGAGCCAGAGACATGGAACTCTTTGAGGAAAAGTTCTCAGATG 859
Db 109 ATGGCATCAGTATACCTGAGCCAGAGACATGGAACTCTTTGAGGAAAAGTTCTCAGATG 168
QY 860 TTCATCTGTGGCTCTGAACCTTCAAGGGGTCTCTGAAGATGAATCCAGATGACAGAT 919
Db 169 TTCATCTGTGGCTCTGAACCTTCAAGGGGTCTCTGAAGATGAATCCAGATGACAGAT 228
QY 920 TAACCTGTTCCTCAACTCTGGAGAGCTCTTACTTTGATTTTCAAGAGGCCCAATTA 979
Db 229 TAACCTGTTCCTCAACTCTGGAGAGCTCTTACTTTGATTTTCAAGAGGCCCAATTA 288
QY 980 AAGAAAAGCACGTATGAGGAGGAGAAACAGAGACGCCAACAGGTACTTCCGCTCAAAA 1039
Db 289 AAGAAAAGCACGTATGAGGAGGAGAAACAGAGACGCCAACAGRWWCWDMBGYTSVCWV 348

Search completed: April 22, 2005, 04:37:03
Job time : 2026.2 secs

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:26:40 ; Search time 3325.85 Seconds
(without alignments)
11914.206 Million cell updates/sec

Title: US-10-766-691-9
Perfect score: 1041
Sequence: 1 atggaagaatgataaaatt.....aggtacttcgcctcaaaagt 1041

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	480.6	46.2	695	6	CB169554 RUC603000
2	405	38.9	670	6	BY733578 BY733578
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4	333.6	32.0	500	1	AI385966 ml34h09.y
5	331	31.8	1691	3	AK016781 Mus muscu
6	316.8	30.4	757	7	CK482747 AGENCOURT
7	316.8	30.4	938	1	AA061797 ml34h09.r
8	306.8	29.5	598	2	AV986182 AV986182
9	298.4	28.7	824	5	BU221831 603750354
10	295.6	28.4	536	5	BU686325 UI-CF-DUI
11	289.2	27.8	597	5	BP016186 BP016186
12	284.6	27.3	825	6	CB315094 AGENCOURT
13	269.8	25.9	565	6	CB400506 OSTF177F1
14	258.6	24.8	731	2	AW106692 um32d03.y
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16	252	24.2	494	9	CG538295 VCS3b05.r
17	249	23.9	508	4	BL511582 BBL160006A
18	248.8	23.9	806	7	CK472415 AGENCOURT
19	247.6	23.8	504	5	BX304025 BX304025
20	243.8	23.4	1956	3	AY383681 Rattus no
21	239	23.0	485	2	AV960213 AV960213
22	238.2	22.9	722	7	CK237628 AGENCOURT
23	230.2	22.1	1462	9	AY412140 Homo sapi
24	223.8	21.5	688	5	BW241505 BW241505

25	221.8	21.3	2572	3	AK030598
26	213.4	20.5	570	4	BJ000534
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28	212.8	20.4	642	5	BW336241
29	212.2	20.4	790	7	CK597959
30	212	20.4	1462	9	AY412141
31	210.8	20.2	627	6	BY716459
32	210.6	20.2	500	5	BP187523
33	210.2	20.2	580	7	CO538154
34	209.8	20.2	579	2	AW233105
35	209.4	20.1	380	5	BY075395
36	202.2	19.4	2005	3	AK090045
37	202.2	19.4	2769	3	AK045036
38	200.6	19.3	1893	3	AK050990
39	199.6	19.2	600	5	BW352155
40	199	19.1	295	1	AA626859
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45	190	18.3	754	7	CK358920

ALIGNMENTS

RESULT 1
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LOCUS RUC603000752.R1 CSEQFXN20 testes Bos taurus cDNA, mRNA sequence.
DEFINITION CB169554
ACCESSION CB169554
VERSION CB169554.1 GI:28155681
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 695)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Bovine ESTs (Adelson and Gill)
JOURNAL Unpublished (2003)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
1..695
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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NotI; Site_2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GCCAATTCGAGCTCCACCGGTCGGCGCGCGCTCGAG. Sequence 3' of
the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
normalized Rd 1 library, sequenced 3' with M13R primer."

FEATURES
source
Query Match 46.2%; Score 480.6; DB 6; Length 695;
Best Local Similarity 92.8%; Pred. No. 5.4e-97;
Matches 504; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

ORIGIN

1 ATGGAAGATGAAAAATTAGCTTAAGCTGGAGAGGGTCTTATGGGTGTATTCAA 60
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543 ATGGGAAGATGAAAAATTAGCTTAAGCTGGAGAGGGTCTTATGGGTGTATTCAA 484

QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 DB |||||
 483 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 424
 QY 121 GATCTGTTGTTAGAAAATAGCACTAAGAGAAATACGTATGTTTGAAGCAATTTAAACAT 180
 DB |||||
 423 GATCTGTTGTTAGAAAATAGCTCTTAAGAGAAATACGATGTTTAAAGCAATTTAAACAT 364
 QY 181 CCAATCTGTTGAACCTCATCGAGTGTTCAGGAGAGAAAAGAAAATGTCATTTAGTTT 240
 DB |||||
 363 CCAATCTGTTGAACCTCATTCAGGAGTGTTCAGGAGAGAAAAGAAAATGTCATTTAGTTT 304
 QY 241 GAATCTGTTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 DB |||||
 303 GAGTACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 244
 QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTGCATATACAT 360
 DB |||||
 243 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTCAACTTCTGTGCATATACAT 184
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAAGGAATATC 420
 DB |||||
 183 AATTGTATTACAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAAGGAATATC 124
 QY 421 AAGATTGTGACTTGGGTTTGCACAAATTTGATCCAGAGATGCTACACCGATTAT 480
 DB |||||
 123 AAGATTGTGACTTGGGTTTGCACAAATTTGATCCAGAGATGCTACACCGATTAT 64
 QY 481 GTAGTACAGAGATGTCACGAGTCTTCAACTTCTTGTGGAGATATCTAGTATGTTCT 540
 DB |||||
 63 GTGCTAAGATGTTGACCGAGTCTCCGACCTTCTTGTGGGGATACCCAGTATGTTCT 4
 QY 541 TCA 543
 DB |||||
 3 TCA 1

RESULT 2

BY733578

LOCUS

DEFINITION

BY733578 RIKEN full-length enriched, 16 days neonate male

diencephalon Mus musculus cDNA clone G630052E12 5', mRNA sequence.

BY733578.1 GI:27146705

EST.

Mus musculus (house mouse)

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 670)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,

Sandelin, A., Schneider, C., Sempke, C. A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L. G., Wahlstedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Contact: Yoshihide Hayashizaki
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 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Sphiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-resescgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Fukuda, S., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Adachi, J., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

Location/Qualifiers
 1..670
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 /mol_type="mRNA"
 /strain="C57BL/6J"
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 /clone="G630052E12"
 /sex="male"
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ORIGIN

Query Match 38.9%; Score 405; DB 6; Length 670;
 Best Local Similarity 85.6%; Pred. No. 4.6e-80;
 Matches 450; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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 DB 145 ATGGAAGATGATGAAAAATAGCTAAGACTGAGAGAGGCTCTTATGGGCTGTTATCAAG 204
 QY 61 TCAGAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 DB 205 TCAGAGAAACAAACCTCTCTGGCAAGTAGTAGCGATCAAAAAATTTGTGGAATCTGAAGAT 264
 QY 121 GATCTGTTGTTAGAAAATAGCACTAAGAGAAATACGTATGTTTGAAGCAATTTAAACAT 180
 DB 265 GATCTGTTGTTAGAAAATAGCACTTCCGGGAAATCCGTATGCTGAAGCAGTTGAACAC 324


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QY 361 AACTGTATTCACAGAGATATAAACCTGAAAAATTCTTAATACTAAGCAAGGAATAATC 420
Db 529 AATTGTATTTCATCGGATGTAAACCTGAAACATCTTAATACCAAGCAGGGATGANT 588
QY 421 AAGATTGTGACTTCGGTTGGTTCACAAATCTGATTCAGGAGATGCCCTACACCGATTAT 480
Db 589 AAGATTGTGACTTCGGTTGGTTCACCAATCTTAATTNCA-GAGACGCTTACACANGACTA 647
QY 481 GTAGCTACGAGATGGTACCGAGCTCTCGA 509
Db 648 TGTGCCACCAGTGGTACCGAGCCCCCGA 676

RESULT 4
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LOCUS ml34h09.y1 Stratagene mouse testis (#937308) Mus musculus cDNA
DEFINITION clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN
KINASE KKIALRE (HUMAN); mRNA sequence.
ACCESSION AI385966
VERSION AI385966.1 GI:4199429
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 500)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307801
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 339.
FEATURES
source
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/sex="males"
/tissue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse testis (#937308)"
/note="Organ: testis; Vector: pBluescript SK-; Site: 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCAGTGTCTTTTCTTTT 3'"

ORIGIN
Query Match 32.0%; Score 333.6; DB 1; Length 500;
Best Local Similarity 82.3%; Pred. No. 4.4e-64;
Matches 408; Conservative 0; Mismatches 84; Indels 4; Gaps 2;
QY 135 GAAATAGCACTAAGAGAAATACGTATGTGTGAAGCAATTAACATCCAAATCTTGTGAA 194

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Db 2 GAAATAGCCCTGCGGAAATCCGTATGCTCAAG---TTGAAACACCCAAACCTCGTGAA 58
QY 195 CCTCATCGAGGTGTTTCAGGAGAAAAGAAAATGCAATTTAGTTTGTGAATACTGTGATCA 254
Db 59 CCTCATCGAGGTGTTTCAGGAGAAAAGAAAATGCAATTTAGTTTGTGAATACTGTGATCA 118
QY 255 TACACTTTTAAATGAGCTGGAAAGAAACCCCAATGGAGTTGCTGATGGAGTGATCAAAAG 314
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QY 375 AGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATCAAGATTTGTGACTT 434
Db 239 GGATGTAACACCTGAAACATCTTAATAACCAAGCAAGGATGATAAGATTTGTGACTT 298
QY 435 CGGGTTTGCACAAATTTCTGATTCAGGAGATGCTTACACCGATTAATGATGATGAGATG 494
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QY 495 GTACCGAGCTCTGAACTTCTTGTGGGAGATACCTCAGTATGTTTCTTCACTGCGATATATG 554
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QY 615 AGATGTGGACCAACTT 630
Db 478 CGAGTGGACCACTT 493

RESULT 5
AI385966 1691 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult male testis cDNA, RIKEN full-length enriched
DEFINITION library, clone:4933411017 product:cyclin-dependent kinase-like 1
(CDC2-related kinase), full insert sequence.
ACCESSION AK016781
VERSION AK016781.1 GI:12855701
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE PUBMED 10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL 20499374
MEDLINE PUBMED 11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, I., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

```


Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14977 row: e column: 07
High quality sequence stop: 695.
Location/Qualifiers
1..757
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7110321"
/tissue_type="kidney, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 235"
/note="Organ: kidney; Vector: pExpress-1; Site 1: EcoI
Site 2: NotI; RNA obtained from pooled kidney tissue
a mix of male and female animals at 8 wk old. Tissues
snap-frozen before RNA extraction and purification
(TRI-reagent method). cDNA was primed using oligo-dT
primer: 5'-pGCTAGTCTGATGCGAGCGCGCCCTT25-3', and
cloned into the EcoRV/NotI sites of pExpress-1.
Size-selection >1.4kb resulted in an average insert s
of 2.2 kb. This primary library is non-normalized
(normalized primary library is NIH MGC 236) and was
constructed by Express Genomics (Frederick, MD). Note
this is a NIH MGC library."

Query Match	30.4%;	Score 316.8;	DB 7;	Length 757;	
Best Local Similarity	70.4%;	Pred. No. 2.5e-60;			
Matches 439;	Conservative	0;	Mismatches 182;	Indels 3;	Gaps 1
Qy	1	ATGGAAAAAGTATGAAAAAATTAGCTAAGACTCGAGAAGGCTCTTATGGGGTGTGATTCAAA	60		
Db	103	ATGGAAAAAATCGAAAAAATTTGGAAGAAGTTGGAAGAAGTTCTCTATGGGTAGTGTTCAG	162		
Qy	61	TGCAGAAACAAAACCTCTGGSACAAGTAGCTGTTAAAAAATTTGTGGAATCTCTGAAGAT	120		
Db	163	TGCAGAAACAGAGACACGGTTCAGATCGTGGCCATCAGAGGTTTCTGGAACCGAAGAT	222		
Qy	121	GATCCTGTTGTAGAAAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACCAAT	180		
Db	223	GACCTGTGCATAAAGAAAAATCGCCCTTCAGAAATCCGATGCTCAAGCACTCAAGCAT	282		
Qy	181	CCAAATCTGTGAACTTCATCGAGGTGTTACGGAGAAAAAGGAAAAATGCAATTTAGTTTTT	240		
Db	283	CCCAACTCGTTCAGCCTCTCTGGAAGTCTTCCGCGAGGAGCGCGGCTTCACCTGGTGTC	342		
Qy	241	GAATPACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGGCTGAT	300		
Db	343	GAGTACTGCCACCACACCGTGCTTCAAGCTGGACAGATATCAGAGGGGGGTACCAAGAG	402		
Qy	301	GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCAATATACAT	360		
Db	403	CCTCTCGTGAAGAACATAACTTGGCAGACACTGCAGGCTGTGAATTTCTGCCATAAACAC	462		
Qy	361	AACGTATTACACAGAGATATAAACTCGAAAAATTTCTAATACAGCAAGGAATATC	420		
Db	463	AAC TGCAATACAGAGATGTGAAGCGGGAACAACTTCTCATCAACCAACACTCAGTCATT	522		
Qy	421	AAGATTGTGACTTTCGGGTTTGCACAAAATCTGATT-- --CCAGAGATGCTCACCCGAT	477		
Db	523	AAGCTCTGTGACTTTGGGTTTGCAGGCCTTCTCACTGGACCTGCTGACTACTACACTGAC	582		
Qy	478	TATGTAGTACAGAGATGGTACCGAGTCTCGAACTTCTTGTGGGAGATACCTAGTATGGT	537		

Db	583	TACGTGGCCACAGTGTGACCGCTCACCTGAGTGTCTAGTGGGAGACACAGATATGCG	642
Qy	538	TCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTGTCAGAGCTCCTCACAGGCCAGCCA	597
Db	643	CCCCAGTAGATGTCCTGGGCAATGGGTGTGTGTTGTGAGTTCCTGTCCGGAGTGCTT	702
Qy	598	CTGTGGCCTGAAAAATCAGATGTG	621
Db	703	CTGTGGCCAGGAAAAATCGAATGTG	726

FEATURES	Location/Qualifiers	RESULT 7
source	1. .757	AA061797
High quality sequence stop: 695.		

LOCUS	AA061797	938 bp	linear	EST 03-FEB-1997
DEFINITION	m33409.1 Stratiogene mouse testis (#937308) Mus musculus cDNA clone IMAGE:513953 5', similar to gb:X66358 SERINE/THREONINE-PROTEIN KINASE KIALRE (HUMAN); mRNA sequence.			

ACCESSION AA061797
VERSION AA061797.1
KEYWORDS ECT GI:1555606

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REFERENCES
AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the State in the Development of the Economy	Journal of Economic Surveys	1998, 12(4), 481-510
2. The Impact of the Internet on the Labor Market	Journal of Labor Economics	1999, 17(2), 181-200
3. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2000, 18(2), 181-200
4. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2001, 19(2), 181-200
5. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2002, 20(2), 181-200
6. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2003, 21(2), 181-200
7. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2004, 22(2), 181-200
8. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2005, 23(2), 181-200
9. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2006, 24(2), 181-200
10. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2007, 25(2), 181-200
11. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2008, 26(2), 181-200
12. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2009, 27(2), 181-200
13. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2010, 28(2), 181-200
14. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2011, 29(2), 181-200
15. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2012, 30(2), 181-200
16. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2013, 31(2), 181-200
17. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2014, 32(2), 181-200
18. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2015, 33(2), 181-200
19. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2016, 34(2), 181-200
20. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2017, 35(2), 181-200
21. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2018, 36(2), 181-200
22. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2019, 37(2), 181-200
23. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2020, 38(2), 181-200
24. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2021, 39(2), 181-200
25. The Effect of the Internet on the Labor Market: A Review of the Literature	Journal of Labor Economics	2022, 40(2), 181-200

ORIGIN

Query Match	30.4%;	Score 316.8;	DB 7;	Length 757;
Best Local Similarity	70.4%;	Pred. No. 2.5e-60;		
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Db	163	TGCAGAAACAGAGACACGGGTCAGTCTGTGGCCATCAAGAGGTTTCTGGAACCGGAAGAT	222
QY	121	GATCCTGTGTTAGAAAAATAGCACTAAGAGAAATACGTATGTTTGAAGCAATTAAAAACAT	180
Db	223	GACCCTGTGCATAAAGAAAAATCGCCCTTCGAGAAATCCGATGCTCAAGCAACTCAAGCAT	282
QY	181	CCAAATCTTGTGAACCTCATCGAGGTGTTTCAAGGAGAAAAAGGAAAAATGCATTTAGTGT	240
Db	283	CCCAACCTCGTCAGCCTCCTGGAAGTCTTCCGCGAGGAAGCGCGGCTTACCTGGTGTC	342
QY	241	GAATACTGTGNTATACACTTTTAAATGAGTGTGAAAGAAACCCAAATGGAGTTGCTGAT	300
Db	343	GAGTACTTGCCACCACACGGTGCTTCACGAGCTGCACAGATATCAGAGGGGGTACACAG	402
QY	301	GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGCATATACAT	360
Db	403	CCTCTCGTGAAGAACATAAATTCGCGACACTGCAGGCTGTGAATTTCTGCCATTAACAC	462
QY	361	AACGTATTTCACAGAGATATAAAACCTGAAAAATTTCTATAACTAAGCAAGGAATAATC	420
Db	463	AACGTGCATACAGAGATGTGAAGCGCGAAAAACATTTCTCATCCCAACCACTCAGTCATT	522
QY	421	AAGATTGTGACTTCGGGTTTGGCACAAATTTCTGATT---CCAGGAGATGCCTACCCGAT	477
Db	523	AAGCTCTGTGACTTTGGGTTTGGACGGCTTCTCACTGGACCTGGTGACTACTACACTGAC	582
QY	478	TATGTAGTACGAGATGGTACCGAGCTCCGAACTCTTCTGTGGAGATATCTAGTATGGT	537

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307801

FEATURES
source

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Location/Qualifiers
1. 938
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
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/sex="males"
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/dev_stage="10-12 week ob
/lab_host="SOUR (Xanagyc
/clone_lib="Stratagene m
/notes="organ: testis; Vec
EcoRI; Site 2: XhoI; Clon
Oligo dT. Average insert
~5' adaptor sequence; 5'
sequence: 5' CTCGAGTTT

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ORIGIN

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Best Local Similarity	84.9%	Pred. No. 2.5e-60;		
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2Y	135	GAAAATAGCACTAGAGAAATACGTATGTTGGAACAAATTAACACATCCAAATCTGTGAA	194	
1		GAATATACCTCCGGGAAATCCGTATGCTGAAG---TTGAACACCCAAACCTCGTAA	57	
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FEATURES
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	Query Match	29.5%	Score 306.8	DB 2	Length 598
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Qy	11	ATGAAAATTAGCTTAAGACTCGAGAGGGTCTTATGGGGTTGTATTCAAATGCGAACA	70		
Db	1	ATGAGAAGATAGGTAAGATAGCGAAGGATCTTATGGCATTTGTGTTTAAATGTCGAACC	60		
Qy	71	AAACCTCTGGAACAAGTAGTAGCTGTTTAAAAAATTTGTGGAAATCTGAAGATGATCTGTGT	130		
Db	61	GTGACTCGGGAACAAATTTGTGGCCATCAAAAAATTTGTGAGTCAGAAGATGACCCGCTGA	120		

Qy	131	TTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATATAAAACATCCAATCTTG	190
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Qy	191	TGAACCTCATCGAGGTGTTCAAGAGAAAAAGGAAAAATGCAATTTAGTTTTTGAAATACTGTG	250
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Qy	251	ATCATACATTTTAAATAGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCA	310
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Qy	311	AAAGCGTATTATGGCAACAACCTTCAAGCTCTTAAATTTCTGTGCATATACATAACTCTGATTTC	370
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Qy	371	ACGAGATATAAAACCTGAAAAATTTCTTAATCACTAAAGCAAGGAATAATCAAGATTTGTG	430
Db	361	ATCGTGATGTAAACCAACGAGAAACATATTAATCACTAAGCAAGGTGTTATCAAGTTGTGTG	420
Qy	431	ACTTCGGGTTTGCACAAAATCTGA--TTCCAGGAGATGCCCTACACCGATTTATGTAGCTA	487
Db	421	ACTTTGGAATTGCAAGAAATTTAACTGGTCTCTGGCGACGATTACACCGACTATGTGGCCA	480
Qy	488	CGAGATGGTACCGAGCTCCTGAACTTTCTGTGGGAGATACCTCAGTATGGTCTTTCAGTCG	547
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RESULT	9
BU221831	
LOCUS	824 bp mRNA linear EST 25-NOV-2002
DEFINITION	CSEQCHN04 Gallus gallus cDNA clone CHEST661l13 5', mRNA sequence.
ACCESSION	BU221831
VERSION	BU221831.1 GI:25410266

REFERENCE
1 (bases 1 to 824)
AUTHORS Boardman, P.E., Sanz-Esquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

12443392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

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FEATURES
source
Location/Qualifiers
1. .824
/organism="Gallus gallus"
/mol_type="mRNA"
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/db_xref="taxon:9031"
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/note="Organ: whole embryo; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match	28.7%;	Score 298.4;	DB 5;	Length 824;
Best Local Similarity	68.7%;	Pred. No. 3.3e-56;		
Matches	426;	Conservative 0;	Mismatches 191;	Indels 3; Gaps 1;

QY	40	TCTTATGGGGTGTATTCAAATCGCAAAACAACTCTGGACAAGTAGTACGCTTTAAA	99
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QY	100	AAATTGTGGAATCTGAAGATGATCTGTGTTTAAAGAAAATAGCACTAAGAGAAATACGT	159
Db	62	AAATTGTGGAATCTGAAGATGATCTGTGTTTAAAGAAAATAGCACTAAGAGAAATACGT	159
QY	160	ATGTTGAAGCAATTAATAACATCAATCTGTGACCTTCATCGAGTGTTCAGGAGAAA	219
Db	122	ATGCTGAGCACTGAACACCCCACTGTGTAACCTGTGGAGGTGTTTCAAGGAAAG	181
QY	220	AGGAAATGATTTAGTTTGAATCTGTGATCATACATCTTTTAAATGAGCTGGAAGA	279
Db	182	AGGAAATGATTTAGTTTGAATCTGTGATCATACATCTTTTAAATGAGCTGGAAGA	279
QY	280	AACTTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	339
Db	242	CACTTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	339
QY	340	CTTAATTTCTGTATATACATCACTGATGATGATGATGATGATGATGATGATGATGAT	399
Db	302	GTGAATTTCTGTATATACATCACTGATGATGATGATGATGATGATGATGATGATGAT	361
QY	400	ATACTAGCAAGGATTAATCAAGATTTGATGATGATGATGATGATGATGATGATGATGAT	456
Db	362	ATACTAGCAAGGATTAATCAAGATTTGATGATGATGATGATGATGATGATGATGATGAT	456
QY	457	CCAGGAGATGCTTACCGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT	421
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QY	517	GTGGGAGATCTAGTATGTTTCTAGTATGATGATGATGATGATGATGATGATGATGATGAT	576
Db	482	GTGGGAGATCTAGTATGTTTCTAGTATGATGATGATGATGATGATGATGATGATGATGAT	576
QY	577	GAGCTCTGACGAGCGGACCTGTCGCTGGAATCAATGATGATGATGATGATGATGATGAT	636
Db	542	GAGCTCTGTCGCGGGTGCCTGTCGCTGGAATCAATGATGATGATGATGATGATGATGAT	636
QY	637	ATAATCAAGACACTAGTAGA	656
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 BU686325
 VERSION
 BU686325.1 GI:23541120
 KEYWORDS
 EST.

SOURCE ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 536)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES source

Location/Qualifiers
 1. 536
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-DUI-adn-i-10-0-UI"
 /tissue_type="Primary Lung Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-DUI"
 /note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-DUI is a normalized cDNA library containing the
 following tissue(s): Primary Lung Epithelial Cells The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into p773-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GGCTGTAGGC.
 TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG LIB=UI-CF-DUI
 TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match	28.4%;	Score 295.6;	DB 5;	Length 536;
Best Local Similarity	98.7%;	Pred No. 1.4e-55;		
Matches	298;	Conservative 0;	Mismatches 4;	Indels 0; Gaps 0;

QY	740	GAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCC	799
Db	477	GAACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCC	418
QY	800	ATGGCATCAGTATACCTGAGCCAGACATGGAACCTCTGAGAAAGTTCACAGATG	859
Db	417	ATGGCATCAGTATACCTGAGCCAGACATGGAACCTCTGAGAAAGTTCACAGATG	358
QY	860	TTCAATCTGTGGCTCTGAACCTTCAATGAAGGGGTCTCTCAAGATGAATCCAGATGACAGAT	919
Db	357	TTCAATCTGTGGCTCTGAACCTTCAATGAAGGGGTCTCTCAAGATGAATCCAGATGACAGAT	298
QY	920	TAACTGTGTCCCACTCTCGGAGAGCTCTACTTGTGATCTTTTCAAGAGGCCCAATTA	979

```

Db      297  TAACCTGTTCCCAACTCTCGAGAGCTCTACTTTGATCTTTTCAAGAGGCCCAATTA 238
Qy      980  AAGAGAAAGCAGTAATGAAGAGAGAAACAGAGACGCCACAGGTACTTCCGCTCAAAA 1039
Db      237  AAGAGAAAGCAGTAATGAAGAGAGAAACAGAGAGGCCACAGGTACTTCCGCTCAAAA 178
Qy      1040  GT 1041
Db      177  GT 176

RESULT 11
LOCUS   BP016186
DEFINITION BP016186 Nori Satoh unpublished cDNA library, young adult Ciona
EST 15-MAR-2002
ACCESSION BP016186
VERSION   BP016186.1 GI:19507663
KEYWORDS EST.
SOURCE   Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 597)
Satoch.N., Satoch.Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoch@ascidian.zool.kyoto-u.ac.jp.

FEATURES             source
    source
    1..597
        /organism="Ciona intestinalis"
        /mol_type="mRNA"
        /db_xref="taxon:7719"
        /clone="ciad64e08"
        /tissue_type="whole animal"
        /dev_stage="young adult"
        /clone_lib="Nori Satoh unpublished cDNA library, young
        adult"

ORIGIN
Query Match      27.8%; Score 289.2; DB 5; Length 597;
Best Local Similarity 71.0%; Pred. No. 3.8e-54;
Matches 397; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

Qy      2  TGAAGAAAGTATGAAATAATTAGCTAGAGTGGAGAGGCTCTTATGGGGTTGTATTCAAAAT 61
Db      38  TGGAGAAATATGAGAAATAGTAGTAAAGATAGGAGAGGATCTTATGGCAATGTGTTTAAAT 97
Qy      62  GCAGAAACAAACCTCTGGCAAGTAGTAGCTGTGTAAATAATTTGTGGAATCTGAAGATG 121
Db      98  GTCGGAACCGTGACTCGGGCAAAATTTGGCCATCAAAAAAATTTGTGAGTCAGAAGATG 157
Qy      122  ATCTGTTGTTAGAAATAGCATTAGAGAAATACGTATGTTTGAAGCAATTAAGATC 181
Db      158  ACCCGCTGATCAAGAAATCGCGCTGAGGGAATTCAGAATGTTTAAAGCAATTTGAACACA 217
Qy      182  CAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAAAGGAAATTCATTTAGTTTTCG 241
Db      218  ATAACTTGTGTGAACCTGATTTGAGTTTTCGTCGAAACGCAATTAATACATCTGTGTTCG 277
Qy      242  AATACTGTGATCATACACTTTTAAATGAGCTGGAGAAAGAAACCCCAATGGAGTTGCTGATG 301
Db      278  AGTATTGTGATCATACAGTTTAAATGAAATTGGACAAACACATGAGAGGAGTACCAAGAC 337
Qy      302  GAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGCATATACATA 361

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Db      338  ATCATGTTAAACGTATTGTTTGGCAAGTCTTCAAGCTGTTCACTTTTGCATCAGATA 397
Qy      362  ACTGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATAAATTAAGCAAGGAATAATCA 421
Db      398  ATTGTATACATCGTGATGTAAGAACCCAGAGAACATATTAACTACCTAAGCAAGGTGTATCA 457
Qy      422  AGATTGTGACTTCGGGTTTGCACAAATTTCTGA---TTCCAGGAGATGCCCTACACCGATT 478
Db      458  AGTTGTGTGACTTTGGGATTTTCAAGAAATTTTAACTGGTCTCTGGCGCAGATTTACACCGACT 517
Qy      479  ATGTAGCTTACAGAGATGTTACCGAGCTCTCGAATCTTCTTGTGGGAGATACTCAGTATGTTT 538
Db      518  ATGTGGCCACTAGTGTGTACAGAGCACTGAGCTCTCTGTCGGGACACACTCAGTATGGCC 577
Qy      539  CTTTCAGTCGATATATGGGC 557
Db      578  CTNCAGTGGATGTGTGGGC 596

RESULT 12
LOCUS   CB315094
DEFINITION AGENCOURT 11526413 NICHDR.Rr.Pit1 Rattus norvegicus cDNA clone
IMAGE:6888377 5', mRNA sequence.
ACCESSION CB315094
VERSION   CB315094.1 GI:28838974
KEYWORDS EST.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 825)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC3144 row: i column: 16
High quality sequence stop: 468.
Location/Qualifiers
    1..825
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /db_xref="taxon:10116"
        /clone="IMAGE:6888377"
        /tissue_type="Pituitary"
        /lab_host="DH10B"
        /clone_lib="NICHDR.Rr.Pit1"
        /notes="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; 5'
        and 3' adaptors were used in cloning as follows: 5'
        adaptor sequence: 5'-CACGCCATATGGGC-3' and 3' adaptor
        sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3'
        (where B = A, C, or G and N = A, C, G, or T). Average
        insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies
        contained inserts by PCR. This library was enriched for
        full-length clones and was constructed by Clontech
        Laboratories (Palo Alto, CA)."

ORIGIN
Query Match      27.3%; Score 284.6; DB 6; Length 825;
Best Local Similarity 70.9%; Pred. No. 4.1e-53;
Matches 455; Conservative 0; Mismatches 90; Indels 97; Gaps 2;

Qy      361  AACTGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATAACTAGCAAGGAATAATC 420

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Db 96 AGCTGTATCCATCGGACGTAAACCCGAAACATCTTAATACCCAGACGAGTGATA 155
Qy 421 AAGATTGTGACATCGGTTTGACAAATTCGATTCAGGAGATGCCTACACCGATTAT 480
Db 156 AAGATTGTGACATCGGTTTGACAAATTCGATTCAGGAGATGCCTACACAGACTAT 215
Qy 481 GTAGTACGAGATGGTACCGAGCTCCTGAATCTTGTGCGGAGATCACTAGTATGGTTCT 540
Db 216 GTTCCACACAGGTGGTACCGAGCCCTGAATCTTGTGCGGAGACACGAGTACCGCTCC 275
Qy 541 TCAGTGCATATATGGGCTATGTTGTTTGTGAGAGCTCTCTGACAGCCAGCCACTG 600
Db 276 TCTGTGACATATGGGCTGTGCGCTGTGTTTGTGAGAGCTCTCTGACAGCCAGCCACTG 335
Qy 601 TGGCTTGGAAATCAGATGCGGACCACTTATCTGTAATCAGAACACTAGTAGAGAGC 660
Db 336 TGGCCAGGAAATCAGATGCGGACCACTTATCTGTAATCAGAACACTAGTAGAGAGC 660
Qy 661 GGGTTTGGCCATGTTGACCAAGGCTGGTCTCGAACTCTTGACGTCAGTCAAGTGATCCACCTGCC 720
Db 386 ----- 385
Qy 721 GTAGCTCTCAAGTCTCGAATTACAGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 386 -----GGGAAAGCTGATCCCAAGGCATCAGTCTATCTTT 419
Qy 781 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCGACAGACATCGAACTCTT 840
Db 420 AAAAGTAACCGTTTTTCCGTTGATCAGTATACCTGAGCGACAGACATCGAACTCTT 479
Qy 841 GAGGAAAGTCTCAGATGTTTCACTCTGTGCTCTGAACTTCACTG- AAGGGGTGTCTGAA 899
Db 480 GAAGAAATTCCTCAATGTTTCAGCTATGCTTTAACTTTTCATGAAGGSGTCTGAA 539
Qy 900 GATGAATCAGATGACAGATTAACCTGTTCCCACTCTGAGAGCTCTCTGAGCTCTT 959
Db 540 GATGATCTGATGAGAGCTGACCTGTGCCAGCTGTGGACAGTACCTACTTTCGAGTC 599
Qy 960 TTTTCAAGAGGCCCAATTAAGAAAGAACGACGTAATGAAGG 1001
Db 600 TTTTCAAGAGGCCCAATTAAGAAAGAACGACGTAATGAAGG 641

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RESULT 13
LOCUS CB400506
DEFINITION OSTF17F10_1 AD-wrmcDNA Caenorhabditis elegans cdna, mRNA linear EST 15-MAY-2003
ACCESSION CB400506
VERSION CB400506.1 GI:30742233
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE Rhabditidae; Nematoda; Chromadorea; Rhabditida;
AUTHORS Rebol, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
Tollas, P.P., Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu

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Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu

POLYA=No. Location/Qualifiers
 1. 565
 /organism="Caenorhabditis elegans"
 /mol_type="mRNA"
 /strain="N2"
 /db_xref="taxon:6239"
 /sex="Hermaphrodite and male"
 /tissue_type="whole animal"
 /dev_stage="mixed stage"
 /clone_lib="AD-wrmcDNA"
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

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Query Match 25.9%; Score 269.8; DB 6; Length 565;
Best Local Similarity 67.6%; Pred. No. 8.4e-50;
Matches 379; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 31 GGAAGAGGGTCTTATCGGGTTGTTTCAATTCAGAAACAAACCTCTCGACAAAGTAGTA 90
Db 5 GGTGAAGGGTTCATATGAGTGTGTATATAATGTAAATAATAGGATATCGACAAATTGTG 64
Qy 91 GCGTGTAAATAAATTCGTGGAATCTGAGATGATCTCTGTTTAAAGAAATAGACTAAGA 150
Db 65 GCATCAAAAGTTCGTGGAATCTGAGATGATCTCGCATATTAAGAAATTCGCTACGG 124
Qy 151 GAAATACGTATGTGAAGCAATTAACCAATCTGTGAACCTCATCGAGGTGTTTC 210
Db 125 GAAATCAGAAATCTGAAGCAACTGAAACATCAAAATTTGTTGGATTGATTGAGTGTTC 184
Qy 211 AGGAGAAAGGAAATGCATTTAGTTTGTGAATCTGTGATCATACACTTTTAAATGAG 270
Db 185 AACCGAACCGAAATCTCATCTCTTTGAACTTTGTGATCGAACTGTACTTCACGAG 244
Qy 271 CTGGAAGAAACCCAAATCGAGTGTCTGATGAGTGATCAAAAGCGTATTATGCAACA 330
Db 245 TTGGAGAGAAATCCGCATGGAGTTAACGATGACTCATAGAAATTAATTTATCAATTG 304
Qy 331 CTTCAAGCTCTTAATTTCTGTCATATACATACCTGATTCACAGAGATATAAACTGAA 390
Db 305 CTAGAAGCTCTTAAATTTCTGCACAGTCACAAATGTAATTCATCGAGATGTGAACCGGA 364
Qy 391 AATATTTCTAATAACTAAGCAAGGAATAATCAAGATTTCGTGACTTCGGGTTTGCACAA 450
Db 365 AACATTTCTTGACACGGAATGATCAAGTGAACCTTGGAGATTTCGGATTTCGGAATA 424
Qy 451 CTGATTCAGGAGATGCTACACCGATTATGATGATGATGATGATGATGATGATGATGAT 510
Db 425 ATAAACACGCGGAAATGTATATCTGACTATGTGCAACTCTGTTGATCGAGTGTCCAG 484
Qy 511 CTTCTTGTGGGAGATACCTGATGATGTTTCTTCAGTCGATATATGCGGTATTTGGTGTGT 570
Db 485 CTTCTGTCGGTGATGTTTCAATTTGGGCCACCTGTAGACATTTTGGGCTGTAGGATGTA 544
Qy 571 TTTGAGAGCTCTCTGACAGGC 591
Db 545 TATCGGAGCTGTTGACTGGC 565

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RESULT 14
LOCUS AW106692
DEFINITION

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AW106692 731 bp mRNA linear EST 20-OCT-1999
 um32d03.Y1 Sugano mouse kidney mKia Mus musculus cDNA clone
 IMAGE:2236229 5', similar to gb:X66358 SERINE/THREONINE-PROTEIN
 KINASE KXIALRE (HUMAN);, mRNA sequence.

ACCESSION AW106692
 VERSION AW106692.1 GI:6077492
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 731)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1006441
 Seq primer: custom primer used
 High quality sequence stop: 433.
 Location/Qualifiers
 1..731
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2236229"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse kidney mklia"
 /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTTTGGCTACTGG], digested vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
 ORIGIN
 Query Match 24.8%; Score 258.6; DB 2; Length 731;
 Best Local Similarity 66.9%; Pred. No. 2.7e-47;
 Matches 382; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
 QY 5 AAAAGTATGAAATATTAGTAAAGCTGAGAGGGTCTTATGCGGTGTGTTTCAATGCA 64
 DB |||||
 QY 156 AAATATGAAATATTGGAAGATTGGAAGAGGCTCTATGCGGTGTGTTCAATGCA 215
 DB |||||
 QY 65 GAAACAAACCTCTGGACAAGTAGTGTGTTAAATAATTTGTGGAATCTGAAGATGATC 124
 DB |||||
 QY 216 GAAACAGGGACACGGGTCTGATCGTGGCCATCAAGAGGTTTCTGGAACCGAAGATGACC 275
 DB |||||
 QY 125 CTGTTGTTAAGAAATAGCATTAGAGAAATACGTATGTTGAAGCAATTAACATCCAA 184
 DB |||||
 QY 276 CTGTGTTAAGAAATATGCCCTCTGAGAAATCCGCATGCTCAAGCACTCAAGCACCCCA 335
 DB |||||
 QY 185 ATCTTGTGAACCTCATCAGGTGTTTCAGGAGAGAAAGAAATGCAATTTAGTTTGAAT 244
 DB |||||
 QY 336 ACCTGGTCAACTCTCTGGAAGTCTTCGGAGAGACGGAGGCTTCACCTGGTGTTCAGT 395
 DB |||||
 QY 245 ACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCCAATGGAGTTGCTGATGGAG 304
 DB |||||

Db 396 ACTCGACCAACACGGTGTCTTACAGAGCTGGATCGGTATCAGAGGGGGTACCAAGCCTC 455
 QY |||||
 QY 305 TGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGCATATACATAACT 364
 Db |||||
 Db 456 TCGTGAAGAACAATAACTTGGCAGACACTGCAGGCGTGTAAATTTCTGCCATAAACATAACT 515
 QY |||||
 QY 365 GTATTACAGAGATATATAAACCTGAAAATATTCTAATAACTAAGCAAGGAATATATCAAGA 424
 Db |||||
 Db 516 GCATACACAGAGACGTGAAGCCGAAAATATTCTCATCACCAACAGTCACGCCATTAAGC 575
 QY |||||
 QY 425 TTCTGTACTTCGGGTTTGCACAAATCTGATT---CCAGGAGATGCTTACACCCGATTATG 481
 Db |||||
 Db 576 TCTGTGACTTTGGGTCGCACGGCTCTCTACTGACCAANGTACTACTACACACTACN 635
 QY |||||
 QY 482 TAGCTACGAGATGGTACCGAGCTCTCTGAACCTTCTTGTGGGAGATPACTCAGTATGTTCTT 541
 Db |||||
 Db 636 GTGCCACCCCGTGTACTGTCTCACCCGAGCTGTAGTTGGAGACACGACGATTTGGTCCC 695
 QY |||||
 QY 542 CAGTCGATATATGGGCTATTGTTGTGTTT 572
 Db |||||
 Db 696 CTGTAGATGTCTGGGCAATTGGCTGTGTGT 726

RESULT 15

AA286088

LOCUS

DEFINITION

vc33b05.r1 Barstead MPLRBI Mus musculus cDNA clone IMAGE:776337 5'

similar to gb:X66358 SERINE/THREONINE-PROTEIN KINASE KIALRE

(HUMAN); mRNA sequence.

AA286088

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:469193

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 424.

Location/Qualifiers

1..718

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="IMAGE:776337"

/sex="mixed"

/tissue_type="Kidney"

/dev_stage="6 weeks"

/lab_host="DH10B"

/clone_lib="Barstead MPLRBI"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors
[CATGGATTCCGGTACC], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pTV3 vector.
Library constructed by Bob Barstead."

ORIGIN

Query Match	24.5%	Score 255;	DB 1;	Length 718;
Best Local Similarity	67.9%	Pred. No. 1.7e-46;		
Matches 416;	Conservative 0;	Mismatches 190;	Indels 7;	Gaps 4;

QY	1	ATCGAAAGTATGAAAGTATGCTAGTAAAGTCTGAGAGAGGCTCTTATGGGTCTGATTTCAAA	60
Db	109	ATGGAAGAAATATGAAAGAAATGGAAGATTTGGAAGAGGCTCTATGGGTAGTGTTCAG	168
QY	61	TGCAGAAACAAACCTCTCGACAAGTAGTGTGTTAAAGAAATTTCTGGAATCTGAAGAT	120
Db	169	TGCAGAAACAGGGACACGGGTGATCTGCGGCATCAAGAGGTTTCTGGAAACCGAAGAT	228
QY	121	GATCCTGTTGTTAAGAAATAGCACTTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT	180
Db	229	GACCTGTGTCATAAGAAAGAAATCGCCCTTCGAGAAATCCGCACTCTCAAGCACTCAAGCAC	288
QY	181	CCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAAAGAAAGAAATGCAATTTAGTTTTT	240
Db	289	CCCAACCTGTCTCACTCTCGAAGTCTTCCGAG- AAGCGGAGGCTTCACCTGGTGTTC	347
QY	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	300
Db	348	GAGTACTGCGACCAACAGGTGCTTCACGAGCTGGATCGGTA-TCAGAGGGGGTACAGAG	406
QY	301	GGAGTGATCAAGAGGTATTTATGGCAACACTTCAAGCTCTTAATTAATTAAGCAAGGAATATC	360
Db	407	CCTCTCGTGAAGAACATAAATTTGGCAGACACTGCAAGGCTGTAAATTTCTGCCATAAAT	466
QY	361	AACTGTATTCACAGAGATATAAACCCTGAATATTTCTTAATTAATTAAGCAAGGAATATC	420
Db	467	AACTGCATACACAGAGAGCTGAGCCGGAATATTTCTTATTAACCAAGTCAGCCATT	526
QY	421	AAGATTGTGACTTCGGGTTTGCA- ---CAAATTCGTATTCAGGAGATGCTACACCGA	476
Db	527	AAGCTCTGTGACTTTGGGGTTTCGAACGGCTTCTCACTGGACCAAGTGAATCTACTACACGA	586
QY	477	TTATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTTGTGGGAGATCTCAGTATGG	536
Db	587	CTACGTGGCCACCCGGTGGTACCGGTCAACCGAGCTGCTAGTGGGAGACACGCGAGTATGG	646
QY	537	TTCTTCAGTCGATATATGGGCTATTTGGTTGTGTTTTTTCAGAGCTCCTGACAGCCAGCC	596
Db	647	TCCCCCTGTAGATGCTGGGC- AATGGCTGTGTGTTTGTGAGTTACTGTCCGAGTGCC	705
QY	597	ACTGTGGCCTGGA	609
Db	706	TCTATGGCAAGGA	718

Search completed: April 22, 2005, 01:23:04
Job time : 3334.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 23:37:20 ; Search time 3944.37 Seconds
(without alignments)
1602.273 Million cell updates/sec

Title: US-10-766-691-9

Perfect score: 1041

Sequence: 1 atggaagaagtataaaatt.....aggtacttcgcgtcaaaagt 1041

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1041	100.0	1041	US-10-766-691-9	Sequence 9, Appli
2	1025	98.5	1068	US-10-766-691-3	Sequence 3, Appli
3	839	80.6	945	US-10-766-691-11	Sequence 11, Appli
4	823	79.1	972	US-10-766-691-5	Sequence 5, Appli
5	821	78.9	1790	US-10-333-314-30	Sequence 30, Appli
6	762.8	73.3	1678	US-10-250-889-6	Sequence 6, Appli
7	709	68.1	1819	US-10-766-691-13	Sequence 13, Appli
8	645.6	62.0	887	US-09-834-496A-3	Sequence 3, Appli
9	645.6	62.0	882	US-09-834-496A-1	Sequence 1, Appli
10	454.4	43.7	561	US-10-766-691-1	Sequence 1, Appli
11	454.4	43.7	594	US-10-766-691-7	Sequence 7, Appli

12 343.8 33.0 1363 10 US-09-960-706-1079 Sequence 1079, Ap
13 343.8 33.0 1612 17 US-10-363-616-146 Sequence 146, App
14 343.8 33.0 2944 18 US-10-357-930-24573 Sequence 24573, A
15 251.8 24.2 1701 16 US-10-174-794-5 Sequence 5, Appli
16 251.8 24.2 3080 16 US-10-174-794-3 Sequence 3, Appli
17 241.2 23.2 2095 17 US-10-369-022-21 Sequence 21, Appli
18 241.2 23.2 2095 18 US-10-757-262-107 Sequence 107, App
19 202.6 19.5 1513 18 US-10-620-052A-33 Sequence 33, Appli
20 162 15.6 1635 14 US-10-072-036-112 Sequence 112, App
21 162 15.6 1635 14 US-10-072-036-114 Sequence 114, App
22 161.6 15.5 1297 11 US-09-969-034-4494 Sequence 4494, Ap
23 161.6 15.5 1297 16 US-10-295-681-28 Sequence 28, Appli
24 160.4 15.4 2213 17 US-10-440-464-137 Sequence 137, App
25 160.4 15.4 2213 17 US-10-641-643-1037 Sequence 1037, Ap
26 160.4 15.4 2734 18 US-10-723-860-7854 Sequence 7854, Ap
27 160 15.4 1322 9 US-09-925-300-324 Sequence 324, App
28 158.4 15.2 1297 16 US-10-295-681-30 Sequence 30, Appli
29 155.6 14.9 2213 16 US-10-295-681-40 Sequence 40, Appli
30 154.2 14.8 1050 9 US-09-954-456-84 Sequence 84, Appli
31 154.2 14.8 1050 9 US-09-954-456-718 Sequence 718, App
32 154.2 14.8 1050 9 US-09-954-456-1165 Sequence 1165, Ap
33 154.2 14.8 1050 11 US-09-968-007A-985 Sequence 985, App
34 154.2 14.8 1050 15 US-10-177-293-40 Sequence 40, Appli
35 154.2 14.8 1050 16 US-10-204-041-7 Sequence 7, Appli
36 154.2 14.8 1050 17 US-10-172-118-668 Sequence 668, App
37 154.2 14.8 1050 17 US-10-189-266-4 Sequence 4, Appli
38 154.2 14.8 1050 17 US-10-342-887-668 Sequence 668, App
39 154.2 14.8 1050 18 US-10-723-860-2447 Sequence 2447, Ap
40 154.2 14.8 1050 19 US-10-843-641A-3111 Sequence 3111, Ap
41 154.2 14.8 1050 19 US-10-843-641A-3745 Sequence 3745, Ap
42 154.2 14.8 1050 19 US-10-843-641A-4192 Sequence 4192, Ap
43 154.2 14.8 1050 19 US-10-843-641A-7455 Sequence 7455, Ap
44 154.2 14.8 1235 18 US-10-733-878-420 Sequence 420, App
45 154.2 14.8 1235 18 US-10-751-736-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-766-691-9
; Sequence 9, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-9

Query Match 100.0%; Score 1041; DB 19; Length 1041;
Best Local Similarity 100.0%; Pred. No. 6.6e-266;
Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGAAGAAGTATAAAATTAGCTAACACGAGAGGCTTATGGGTGTTATCAA 60
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Db 1 ATGAAAAGTATGAAAAATAGCTAGAGCTGGAGAGGCTCTTATGGGTTGTATTCAA 60
QY 61 TGAGAAACAAACCTCTGACAGTAGTAGCTGTAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGAGAAACAAACCTCTGACAGTAGTAGCTGTAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCTGTTGTTAAGAAAATAGCACTTAAGAGAAATACGTATGTTGAAGCAATTAAGAAAT 180
Db 121 GATCTGTTGTTAAGAAAATAGCACTTAAGAGAAATACGTATGTTGAAGCAATTAAGAAAT 180
QY 181 CCAATCTGTTGAACTCTGAGGTTGTCAGAGAAAGGAAATCAATTTAGTTT 240
Db 181 CCAATCTGTTGAACTCTGAGGTTGTCAGAGAAAGGAAATCAATTTAGTTT 240
QY 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGGAGTTCGTAT 300
Db 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGGAGTTCGTAT 300
QY 301 GGAGTGATCAAAAGGTTATGGAACACCTTCAAGCTCTTAATTTCTGTCAATATACAT 360
Db 301 GGAGTGATCAAAAGGTTATGGAACACCTTCAAGCTCTTAATTTCTGTCAATATACAT 360
QY 361 AACTGTATTCAGAGATATTAACCTGAAATATTTCTTAATTAAGCAAGCAATATATC 420
Db 361 AACTGTATTCAGAGATATTAACCTGAAATATTTCTTAATTAAGCAAGCAATATATC 420
QY 421 AAGATTTGTGATCTCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 480
Db 421 AAGATTTGTGATCTCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 480
QY 481 GTAGCTAGAGATGATCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 540
Db 481 GTAGCTAGAGATGATCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 540
QY 541 TCAGTTCGATATATGCGCTATGTTGTTGTTTTCAGAGCTCTTGAAGCAATCAATCAATCTTT 600
Db 541 TCAGTTCGATATATGCGCTATGTTGTTGTTTTCAGAGCTCTTGAAGCAATCAATCAATCTTT 600
QY 601 TGGCTCGAAATCAGATGTGAGCAACCTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 660
Db 601 TGGCTCGAAATCAGATGTGAGCAACCTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 660
QY 661 GGGTTTCGCAATGTTGACAGGCTGCTGAACTCTTGAAGCAATCAATCAATCTTT 720
Db 661 GGGTTTCGCAATGTTGACAGGCTGCTGAACTCTTGAAGCAATCAATCAATCTTT 720
QY 721 GTAGCTCTCAAAAGTGTGGAATTAAGAGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCTCTCAAAAGTGTGGAATTAAGAGAAATTAATCCCAAGACATCAATCAATCTTT 780
QY 781 AAAAGTAAACGGTTTTCATGTCATGTCGAGTCTGAACTCTTGAAGCAATCAATCAATCTTT 840
Db 781 AAAAGTAAACGGTTTTCATGTCATGTCGAGTCTGAACTCTTGAAGCAATCAATCAATCTTT 840
QY 841 GAGGAAAGTTCTCAGATGTTCAATGTCGCTGCTGAACTCTTGAAGCAATCAATCAATCTTT 900
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QY 901 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTTGAAGCAATCAATCAATCTTT 960
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTTGAAGCAATCAATCAATCTTT 960
QY 961 TTTCAAGAGCCCAATTAAGAGAAACGCTTAATGAAGGAGAAACAGAGAGCCCA 1020
Db 961 TTTCAAGAGCCCAATTAAGAGAAACGCTTAATGAAGGAGAAACAGAGAGCCCA 1020
QY 1021 CAGGTACTTCCGCTCAAAAGT 1041
Db 1021 CAGGTACTTCCGCTCAAAAGT 1041
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; Sequence 3, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-3

Query Match 98.5%; Score 1025; DB 19; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1.2e-261;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGAAAAGTATGAAAAATAGCTAGAGCTGGAGAGGCTCTTATGGGTTGTATTCAA 60
Db 1 ATGAAAAGTATGAAAAATAGCTAGAGCTGGAGAGGCTCTTATGGGTTGTATTCAA 60
QY 61 TCAGAAACAAACCTCTCGCAAGTAGTAGCTGTAAAAATTTGTGAACTCTGAAGAT 120
Db 61 TCAGAAACAAACCTCTCGCAAGTAGTAGCTGTAAAAATTTGTGAACTCTGAAGAT 120
QY 121 GATCTGTTGTTAAGAAAATAGCACTTAAGAGAAATACGTATGTTGAAGCAATTAAGAAAT 180
Db 121 GATCTGTTGTTAAGAAAATAGCACTTAAGAGAAATACGTATGTTGAAGCAATTAAGAAAT 180
QY 181 CCAATCTGTTGAACTCTGAGGTTGTCAGAGAAAGGAAATCAATTTAGTTT 240
Db 181 CCAATCTGTTGAACTCTGAGGTTGTCAGAGAAAGGAAATCAATTTAGTTT 240
QY 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGGAGTTCGTAT 300
Db 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGGAGTTCGTAT 300
QY 301 GGAGTGATCAAAAGGTTATGGAACACCTTCAAGCTCTTAATTTCTGTCAATATACAT 360
Db 301 GGAGTGATCAAAAGGTTATGGAACACCTTCAAGCTCTTAATTTCTGTCAATATACAT 360
QY 361 AACTGTATTCAGAGATATTAACCTGAAATATTTCTTAATTAAGCAAGCAATATATC 420
Db 361 AACTGTATTCAGAGATATTAACCTGAAATATTTCTTAATTAAGCAAGCAATATATC 420
QY 421 AAGATTTGTGATCTCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 480
Db 421 AAGATTTGTGATCTCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 480
QY 481 GTAGCTAGAGATGATCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 540
Db 481 GTAGCTAGAGATGATCGGCTTTGCAAAATTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 540
QY 541 TCAGTTCGATATATGCGCTATGTTGTTGTTTTCAGAGCTCTTGAAGCAATCAATCAATCTTT 600
Db 541 TCAGTTCGATATATGCGCTATGTTGTTGTTTTCAGAGCTCTTGAAGCAATCAATCAATCTTT 600
QY 601 TGGCTCGAAATCAGATGTGAGCAACCTTCTGAGAGATGCTTCAAGCTCTTAATTTCTGTCAATATACAT 660
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Qy 661 GGGTTTCCCATGTTGACCGCTGGTCTCGAACTCTTGACGTCAAGTATCCACCTGCC 720
Db 661 GGGTTTCCCATGTTGACCGCTGGTCTCGAACTCTTGACGTCAAGTATCCACCTGCC 720
Qy 721 GTAGCCTCTCAAGTCTGGAATACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCCTCTCAAGTCTGGAATACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Qy 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGAAACTCTT 840
Db 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGAAACTCTT 840
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTCTGAACTTCATGAAGGGGTGCTGAAG 900
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Db 901 ATGAATCCAGATGACAGATTAACTGTTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 960
Qy 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Db 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Qy 1021 CAGGT 1025
Db 1021 CAGGT 1025

RESULT 3
US-10-766-691-11
; Sequence 11, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Lex-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 945
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-11

Query Match 80.6%; Score 839; DB 19; Length 945;
Best Local Similarity 90.8%; Pred. No. 3e-212;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGGAAGATGATAAAATTAAGCTGAGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Db 1 ATGGAAGATGATAAAATTAAGCTGAGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Qy 121 GATCCTCTGTTAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTCTGTTAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
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Qy 181 CCAAACTTTGTGAACCTCATCGAGGTGTTCAAGGAGAAAAAGGAAAAATTCATTTAGTTTTT 240
Db 181 CCAAACTTTGTGAACCTCATCGAGGTGTTCAAGGAGAAAAAGGAAAAATTCATTTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTCGAAATATTCTAATACTAAGCAAGGAATATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTCGAAATATTCTAATACTAAGCAAGGAATATATC 420
Qy 421 AAGATTTGTGACTTTCGGGTTTGGCAAAATTTCTGATTCAGGAGATGCTTACACCGATTAT 480
Db 421 AAGATTTGTGACTTTCGGGTTTGGCAAAATTTCTGATTCAGGAGATGCTTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGGTACCGAGCTTCTGAACTTCTTGTGGGAGATACCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTTCTGAACTTCTTGTGGGAGATACCTCAGTATGGTTCT 540
Qy 541 TCAGTCGATATATGGGCTATTGGTTGGTTTTTTCAGAGCTCTCTGACAGGCCAGCCACTG 600
Db 541 TCAGTCGATATATGGGCTATTGGTTGGTTTTTTCAGAGCTCTCTGACAGGCCAGCCACTG 600
Qy 601 TGGCCTGGAATAACAGATGTGGACCAACTTTATCTGATAATCAACAACACTAGTAGAGACG 660
Db 601 TGGCCTGGAATAACAGATGTGGACCAACTTTATCTGATAATCAACAACACTAGTAGAGACG 660
Qy 661 GGGTTTCCCATGTTGACAGGGCTGGTCTCGAACTCTTGAAGTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCCCATGTTGACAGGGCTGGTCTCGAACTCTTGAAGTCAAGTGATCCACCTGCC 720
Qy 721 GTAGCCTCTCAAGTCTCGGAATTAAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCCTCTCAAGTCTCGGAATTAAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
Qy 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATCGAAACTCTT 840
Db 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATCGAAACTCTT 840
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTCTGAACTTCTGAAGGGGTGCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTCTGAACTTCTGAAGGGGTGCTGAAG 900
Qy 901 ATGAATCCAGATGACAGATTAACTGTTTCCCACTCTCTGAGAGCTCTCTACTTTGATTCT 960
Db 901 ATGAATCCAGATGACAGATTAACTGTTTCCCACTCTCTGAGAGCTCTCTACTTTGATTCT 960
Qy 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Db 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Qy 1021 CAGGTACTTCCGCTCAAAAGT 1041
Db 1021 CAGGTACTTCCGCTCAAAAGT 945

RESULT 4
US-10-766-691-5
; Sequence 5, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
```

; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/10/766,691
 ; CURRENT FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 972
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-766-691-5

Query Match 79.1%; Score 823; DB 19; Length 972;
 Best Local Similarity 90.6%; Pred. No. 5.4e-208;
 Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY	1	ATGGAAGATGATGAAATATAGCTAGACTGAGAGGGTCTTATGGGTTGTATTCAA	60
Db	1	ATGGAAGATGATGAAATATAGCTAGACTGAGAGGGTCTTATGGGTTGTATTCAA	60
QY	61	TGAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAATTTTGTGGAATCTGAAGAT	120
Db	61	TGAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAATTTTGTGGAATCTGAAGAT	120
QY	121	GATCTGTTGTTAAGAAATAGCACTAAGAGAAATACCTATGTTCAAGCAATTAACAT	180
Db	121	GATCTGTTGTTAAGAAATAGCACTAAGAGAAATACCTATGTTCAAGCAATTAACAT	180
QY	181	CCAAATCTGTGAACCTCATGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT	240
Db	181	CCAAATCTGTGAACCTCATGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT	240
QY	241	GAATCTGTGATCATACACTTTTAAATGAGTGTGGAAGAAACCAATGAGTTGCTGAT	300
Db	241	GAATCTGTGATCATACACTTTTAAATGAGTGTGGAAGAAACCAATGAGTTGCTGAT	300
QY	301	GGAGTGATCAAAAGGTTATGTCACAACTTCAAGCTCTTAATTTCTGTCTATATACAT	360
Db	301	GGAGTGATCAAAAGGTTATGTCACAACTTCAAGCTCTTAATTTCTGTCTATATACAT	360
QY	361	AATCTGTTTTCACAGAGATATAAACCCTGAAATATCTTAATTAAGCAAGCAATATC	420
Db	361	AATCTGTTTTCACAGAGATATAAACCCTGAAATATCTTAATTAAGCAAGCAATATC	420
QY	421	AAGATTTGTGACTTCGGGTTTGCAAACTTCCAGGATGCTACACCGATTAT	480
Db	421	AAGATTTGTGACTTCGGGTTTGCAAACTTCCAGGATGCTACACCGATTAT	480
QY	481	GTAGTACGAGATGTTACCGAGTCTCTGACTTCTTTGCGGAGATACAGTATGTTCT	540
Db	481	GTAGTACGAGATGTTACCGAGTCTCTGACTTCTTTGCGGAGATACAGTATGTTCT	540
QY	541	TCAGTGCATATATGGCTATGTTGTTGTTTTCAGAGCTCTGACAGCCGACCTG	600
Db	541	TCAGTGCATATATGGCTATGTTGTTGTTTTCAGAGCTCTGACAGCCGACCTG	600
QY	601	TGGCTTGGAAATACAGATGTCGACCACTTATCTGATTAATCAGAACTAGAGACG	660
Db	601	TGGCTTGGAAATACAGATGTCGACCACTTATCTGATTAATCAGAACTAGAGACG	660
QY	661	GGGTTTGGCCATGTTGACCGAGGCTGCTCGAACTCTTGACGTCAAGTATCCCTGCC	720
Db	661	GGGTTTGGCCATGTTGACCGAGGCTGCTCGAACTCTTGACGTCAAGTATCCCTGCC	720
QY	721	GTAGCTCTCAAGTCTGCTGGAATTAAGCAAAATTAATCCCAAGACATCAATCAATCTTT	780
Db	651	AGGAAATTAATCCCAAGACATCAATCAATCTTT	684

QY	781	AAAAGTAAACGGTCTTTCATGGCATCAGTATACCTGAGCCAGACATGGAACCTCTT	840
Db	685	AAAAGTAAACGGTCTTTCATGGCATCAGTATACCTGAGCCAGACATGGAACCTCTT	744
QY	841	GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAGAGCTCTTATGTTCT	900
Db	745	GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAGAGCTCTTATGTTCT	804
QY	901	ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTGAGAGCTCTTATGTTCT	960
Db	805	ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTGAGAGCTCTTATGTTCT	864
QY	961	TTTCAAGAGGCCCAATTTAAAGAGAAAGCAGCTGAATGAAGGAAAGCAAGACGCCAA	1020
Db	865	TTTCAAGAGGCCCAATTTAAAGAGAAAGCAGCTGAATGAAGGAAAGCAAGACGCCAA	924
QY	1021	CAGGT 1025	
Db	925	CAGGT 929	

RESULT 5
 US-10-333-314-30
 ; Sequence 30, Application US/10333314
 ; Publication No. US20030211093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; YUS, Henry
 ; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
 ; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
 ; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
 ; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
 ; APPLICANT: BAUGHN, Mariah R.; TRIBOLEY, Catherine M.
 ; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
 ; APPLICANT: NGUYEN, Daniel B.; LU, Yan
 ; APPLICANT: BURFORD, Neil; LAL, Preeti G.
 ; APPLICANT: DING, Li; YAO, Monique G.
 ; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
 ; APPLICANT: KEARNEY, Liam; LU, Dzung Aina M.
 ; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
 ; APPLICANT: XU, Yuming; WALSH, Roderick T.
 ; APPLICANT: GIEZEN, Kimberly J.; YANG, Junming
 ; APPLICANT: JACKSON, Jennifer L.
 ; TITLE OF INVENTION: HUMAN KINASES
 ; FILE REFERENCE: P1-0162 USN
 ; CURRENT APPLICATION NUMBER: US/10/333,314
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: PCT/US01/23092
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US 60/220,038
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: US 60/222,112
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/222,831
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: US 60/224,729
 ; PRIOR FILING DATE: 2000-08-11
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 30
 ; LENGTH: 1790
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 1698381CB1
 ; US-10-333-314-30

Query Match 78.9%; Score 821; DB 17; Length 1790;
 Best Local Similarity 90.6%; Pred. No. 2.5e-207;
 Matches 927; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 QY 1 ATGGAAGATGATGAAATATAGCTAGACTGAGAGGGTCTTATGGGTTGTATTCAA 60

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Db 239 ATGGAAGATATGAAAAATTAGCTAAGCTGGAGAGGGCTTTATGGGTTGTATTCAA 298
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAAATTTGGAAATCTGAAGAT 120
Db 299 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAAATTTGGAAATCTGAAGAT 358
Qy 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 359 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 418
Qy 181 CCAATCTGTTGAACCTCATCGAGTCTTCAGAGAGAAAGAAATAGCAATTTAGTTTTT 240
Db 419 CCAATCTGTTGAACCTCATCGAGTCTTCAGAGAGAAAGAAATAGCAATTTAGTTTTT 478
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db 479 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 538
Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Db 539 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATATACAT 598
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATTC 420
Db 599 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATTC 658
Qy 421 AAGATTGTGACTTCGGGTTTGCAACAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 659 AAGATTGTGACTTCGGGTTTGCAACAAATCTGATTCAGGAGATGCTACACCGATTAT 718
Qy 481 GTAGCTACGAGATGTTACCGAGCTCTGAACTTCTTGTGGAGATCTCAGTATGGTTCT 540
Db 719 GTAGCTACGAGATGTTACCGAGCTCTGAACTTCTTGTGGAGATCTCAGTATGGTTCT 778
Qy 541 TCAGTCATATATGGGCTATTGGTTGGTTTGTGAGAGTCTCTGAGAGTCTCTGAGCCACCTG 600
Db 779 TCAGTCATATATGGGCTATTGGTTGGTTTGTGAGAGTCTCTGAGAGTCTCTGAGCCACCTG 838
Qy 601 TGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGAGACG 660
Db 839 TGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACT- 888
Qy 661 GGGTTTCGCCATGTTGACCGAGGTGGTCTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
Db 889 ----- 888
Qy 721 GTAGCCTCTCAAAGTGTGGNAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 889 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 922
Qy 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 840
Db 923 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 982
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAAGGGGTGTCTGAAG 900
Db 983 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAAGGGGTGTCTGAAG 1042
Qy 901 ATGAATCCAGATGACAGATTAACTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATCT 960
Db 1043 ATGAATCCAGATGACAGATTAACTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATCT 1102
Qy 961 TTTCAAGAGGCCCAATTTAAAGAAAAAGACGCTTAATGAAGGAAGAAACAGAGACGCGCAA 1020
Db 1103 TTTCAAGAGGCCCAATTTAAAGAAAAAGACGCTTAATGAAGGAAGAAACAGAGACGCGCAA 1162
Qy 1021 CAG 1023
Db 1163 CAG 1165

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RESULT 6
US-10-250-889-6

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; Sequence 6, Application US/10250889
; Publication No. US20040115629A1
; GENERAL INFORMATION:
; APPLICANT: PANZER, Scott R; LINCOLN, Stephen E.;
; APPLICANT: ALTUS, Christina M.; DUFOUR, Gerard E.;
; APPLICANT: JACKSON, Jennifer L.; JONES, Anissa L.;
; APPLICANT: DAM, Tam C.; LIU, Tommy F.;
; APPLICANT: HARRIS, Bernard; FLORES, Vincent Z.;
; APPLICANT: DAFFO, Abel; MARWAHA, Rakesh;
; APPLICANT: CHEN, Alice J.; CHANG, Simon C.;
; APPLICANT: GERSTIN, Jr., Edward H.; PERALTA, Careyana H.;
; APPLICANT: DAVID, Marie H.; LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1195 USN
; CURRENT APPLICATION NUMBER: US/10/250,889
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: PCT/US02/01009
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,864
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/262,207
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,164
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,215
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,102
; PRIOR FILING DATE: 2001-01-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LI:058298.1:2001JAN12
; US-10-250-889-6

Query Match 73.3%; Score 762.8; DB 18; Length 1678;
Best Local Similarity 90.0%; Pred. No. 7.1e-192;
Matches 925; Conservative 0; Mismatches 2; Indels 101; Gaps 6;

Qy 1 ATGGAAGATATCAAAAATTTAGCTAAGCTGGAGAGGGTCTTATGGGTTGTATTCAA 60
Db 131 ATGGAAGATATCAAAAATTTAGCTAAGCTGGAGAGGGTCTTATGGGTTGTATTCAA 190
Qy 61 TGCAGA-AACAAAACCTCTGCAAGTAGTAGCTGTTAAAAAAATTTGTGGAATCTGAAGA 119
Db 191 TGCAGATACAAAACCTCTGCAAGTAGTAGCTGTTAAAAAAATTTGTGGAATCTGAAGA 250
Qy 120 TGATCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAC 178
Db 251 TGATCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAC 310
Qy 179 ATCCAAATCTTGGAACCTCATCGAGTGTTCAGGAGAGAAAGAAATCAATTTAGTTT 238
Db 311 ATCCAAATCTTGGAACCTCATCGAGTGTTCAGGAGAGAAAGAAATCAATTTAGTTT 370
Qy 239 TTGAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTG 298
Db 371 TTGAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTG 430
Qy 299 ATGGAGTGATCAAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATAC 358

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Db 431 ATGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATATAC 490
QY 359 ATAACTGTATTCACAGAGATATAAAACCTGAAATATCTAATAACAAAGCAAGGAATAA 418
Db 491 ATAACTGTATTCACAGAGATATAAAACCTGAAATATCTAATAACAAAGCAAGGAATAA 550
QY 419 TCAAGATTTGTGACTTCCGGGTTTGCAAAATCTGATTCACAGAGATGCTTACACCGATT 478
Db 551 TCAAGATTTGTGACTTCCGGGTTTGCAAAATCTGATTCACAGAGATGCTTACACCGATT 610
QY 479 ATGTAGCTA-CGAGATGTGACGAGCT-CCTGAACCTTCTGTGGAGATCT-CAGTATG 535
Db 611 ATGTAGCTA-CGAGATGTGACGAGCT-CCTGAACCTTCTGTGGAGATCT-CAGTATG 670
QY 536 GTTCTTCAGTCGATATATGCGGTATTTGGTGTGTTTTCAGAGCTTCTGACAGGCCAGC 595
Db 671 GTTCTTCAGTCGATATATGCGGTATTTGGTGTGTTTTCAGAGCTTCTGACAGGCCAGC 730
QY 596 CACTGTGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATATCAGAACACTAGTAG 655
Db 731 CACTGTGGCTTGAATAATCAGATGTGGACCAACTTTATCTGATATCAGAACACT- 785
QY 656 AGACGGGTTTCGCCATGTTGACACAGGCTGTCTCGAACTCTTGACGCTCAAGTGATCCAC 715
Db 786 ----- 785
QY 716 CTGCGTAGCTCTCAAAAGTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCAA 775
Db 786 -----AGAAATTAATCCCAAGACATCAATCAA 814
QY 776 TCTTTAAAGTAAACGGGTTTTCATGCGCATCAGTATACCTGAGCCAGAGACATGGA 835
Db 815 TCTTTAAAGTAAACGGGTTTTCATGCGCATCAGTATACCTGAGCCAGAGACATGGA 874
QY 836 CTCCTGAGGAAAGTCTCAGATGTTTCATCTGTGCTCTGAACTTCTGAGGGGTGTC 895
Db 875 CTCCTGAGGAAAGTCTCAGATGTTTCATCTGTGCTCTGAACTTCTGAGGGGTGTC 934
QY 896 TGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTGAGAGCTCTCTACTTTG 955
Db 935 TGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTGAGAGCTCTCTACTTTG 994
QY 956 ATTCCTTTCAAGAGGCCCAATTAAGAAAGACGTAATGAAGGAAACAGAAAGAC 1015
Db 995 ATTCCTTTCAAGAGGCCCAATTAAGAAAGACGTAATGAAGGAAACAGAAAGAC 1054
QY 1016 GCCAACAG 1023
Db 1055 GCCAACAG 1062

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RESULT 7
US-10-766-691-13
; Sequence 13, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 13
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-13

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Query Match      68.1%; Score 709; DB 19; Length 1819;
Best Local Similarity 77.0%; Pred. No. 1.5e-177;
Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

QY 1 ATGAAAGATATGAAAAATTTAGCTAAGACTGGAAGAGGGTCTTATGGGGTTGTAATCAA 60
Db 138 ATGAAAGATATGAAAAATTTAGCTAAGACTGGAAGAGGGTCTTATGGGGTTGTAATCAA 197
QY 61 TGCAGAAACAAAACCTCTGACCAAGTAGTAGCTGTTTAAATAAATTTGTGNAATCTGAAGAT 120
Db 198 TGCAGAAACAAAACCTCTGACCAAGTAGTAGCTGTTTAAATAAATTTGTGNAATCTGAAGAT 257
QY 121 GATCCTGTTTAAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAATAACAT 180
Db 258 GATCCTGTTTAAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAATAACAT 317
QY 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAAGAGAAAAAGGAAATGCAATTTAGTTT 240
Db 318 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAAGAGAAAAAGGAAATGCAATTTAGTTT 377
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 300
Db 378 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 437
QY 301 GGAGTCAATCAAAAGCGTATTTATGGCAACAATTCAGCTCTTAAATTTCTGTCAATATACAT 360
Db 438 GGAGTCAATCAAAAGCGTATTTATGGCAACAATTCAGCTCTTAAATTTCTGTCAATATACAT 497
QY 361 AAATCTGATTCACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGGATATC 420
Db 498 AAATCTGATTCACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGGATATC 557
QY 421 AGAATTTGAGCTTCGGGTTTGCAAAAATCTG----- 453
Db 558 AGAATTTGAGCTTCGGGTTTGCAAAAATCTGAGTTGGAATTCATCTTCTCTGTTGCC 617
QY 454 ----- 453
Db 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAATCTTTTCTGCAATTCAGAGATTTT 677
QY 454 ----- 453
Db 678 CTCTGGCTTGGATCCATTTGCTGACACAGTGTTCACCATGGGGCCCGAGGCTCATCTGA 737
QY 454 ----- 453
Db 738 ACTTCTGGCTCAAGTGAATCTTCCACCTCGGCTCCCAAGTCTGGAATGCAAGTGTG 797
QY 454 ----- 453
Db 798 AGCCACCGTCCCGAGCCAGATTTTTCACAAACAATACTACTGAGAGCTCAAGAATTTT 857
QY 454 -----ATTCCAGAGATGCTACACC 474
Db 858 TTAGTGGGAACACAATTTTCGAAACAATTTCTTGAGAACGCAATTCAGGAGATGCTACACC 917
QY 475 GATTATGTAGCTACGAGATGATCCCTCCAGCTCTGAACTCTTCTGTGGAGATCTCTAGTAT 534
Db 918 GATTATGTAGCTACGAGATGATCCCTCCAGCTCTGAACTCTTCTGTGGAGATCTCTAGTAT 977
QY 535 GGTTCCTTCAGTCGATATATGCGGTATTTGGTGTGTTTTCAGAGCTCTCTGACAGGCCAG 594
Db 978 GGTTCCTTCAGTCGATATATGCGGTATTTGGTGTGTTTTCAGAGCTCTCTGACAGGCCAG 1037
QY 595 CCACTGTGGCTCGAAAAATCAGATGTGGACCAACTTTATCTGATATCAGAACACTAGTA 654

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Db 1038 CCACTGTGGCTGGAAATCAGATGTGGACCACTTTATCTGATANTCAGAACACTAGTA 1097
Qy 655 GAGACGGGTTTCGCCATGTTTGACACAGCTGGTCTCGAACTCTTTGACGTCAGGTGATCCA 714
Db 1098 GAGACGGGTTTCGCCATGTTTGACACAGCTGGTCTCGAACTCTTTGACGTCAGGTGATCCA 1157
Qy 715 CCTGCCGTAGCCTCTCAAGTGTGGATTAACAGGAAATTAATCCCAAGCATCAATCA 774
Db 1158 CCTGCCGTAGCCTCTCAAGTGTGGATTAACAGGAAATTAATCCCAAGCATCAATCA 1217
Qy 775 ATCTTTAAAGTAACGGGTTTTTCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 834
Db 1218 ATCTTTAAAGTAACGGGTTTTTCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 1277
Qy 835 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGTGT 894
Db 1278 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGTGT 1337
Qy 895 CTGAAGATGATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTACTTTT 954
Db 1338 CTGAAGATGATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTACTTTT 1397
Qy 955 GATCTTTTCAAGAGGCCCAATTTAAAGAAAGCACGTAATGAAGGAAGAAACAGAGA 1014
Db 1398 GATCTTTTCAAGAGGCCCAATTTAAAGAAAGCACGTAATGAAGGAAGAAACAGAGA 1457
Qy 1015 CGCCACACAGGT 1025
Db 1458 CGCCACACAGGT 1468

RESULT 8
US-09-834-496A-3
; Sequence 3, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-496A-3

Query Match 62.0%; Score 645.6; DB 9; Length 687;
Best Local Similarity 99.4%; Pred. No. 6.2e-161;
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGGAAGAATGATGAAAAATAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
Db 1 ATGGAAGAATGATGAAAAATAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
Qy 61 TGCAGAAACAAACCTCTGGCAAGATAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGCAAGATAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Qy 121 GATCCTCTGTTAGAAATAGCACTAAGCAATAGCTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTCTGTTAGAAATAGCACTAAGCAATAGCTATGTTGAAGCAATTAACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Qy 241 GAATACCTGTGATACATACACTTTTAAATGAGCTGGAGAAACCCCAATGGAGTTGCTGAT 300

Db 241 GAATACCTGTGATACATGCACTTTTAAATGAGCTGGAGAAACCCCAATGGAGTTGCTGAT 300
Qy 301 GGAGTGAATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGAATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTCGAAATATCTTAATACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTCGAAATATCTTAATACTAAGCAAGGAATATC 420
Qy 421 AAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGGAGATACCTAGTATGGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGGAGATACCTAGTATGGTTCT 540
Qy 541 TCAGTCATATATGGGCTATTTGGTTGTTTTGTCAGAGCTCTCTGACAGGCCAGCCACTG 600
Db 541 TCAGTCATATATGGGCTATTTGGTTGTTTTGTCAGAGCTCTCTGACAGGCCAGCCACTG 600
Qy 601 TGGCCTGGAAATCAGATGTGGACCACTTTATCTGATATCAAGAACACTAG 652
Db 601 TGGCCTGGAAATCAGATGTGGACCACTTTATCTGATATCAAGAACACTAG 652

RESULT 9
US-09-834-496A-1
; Sequence 1, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (129)...(815)
US-09-834-496A-1

Query Match 62.0%; Score 645.6; DB 9; Length 882;
Best Local Similarity 99.4%; Pred. No. 7e-161;
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGGAAGAATGATGAAAAATAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
Db 129 ATGGAAGAATGATGAAAAATAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 188
Qy 61 TGCAGAAACAAACCTCTGGCAAGATAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 189 TGCAGAAACAAACCTCTGGCAAGATAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 248
Qy 121 GATCCTCTGTTAGAAATAGCACTAAGCAATAGCTATGTTGAAGCAATTAACAT 180
Db 249 GATCCTCTGTTAGAAATAGCACTAAGCAATAGCTATGTTGAAGCAATTAACAT 308
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Db 309 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 368
Qy 241 GAATACCTGTGATACATACACTTTTAAATGAGCTGGAGAAACCCCAATGGAGTTGCTGAT 300

Db 369 GAATACTGTGATCATGCACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 428
QY 301 GGAGTGCATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATATACAT 360
Db 429 GGAGTGCATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATATACAT 488
QY 361 AACTGTATTTCACAGAGATATAAACTGAAATATTTCTAAATCACTAAGCAAGGAATAATC 420
Db 489 AACTGTATTTCACAGAGATATAAACTGAAATATTTCTAAATCACTAAGCAAGGAATAATC 548
QY 421 AAGATTGTGACTTCGGGTTTCACAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
Db 549 AAGATTGTGACTTCGGGTTTCACAAATTTCTGATTCAGAGATGCTTACACCGATTAT 608
QY 481 GTAGCTACGAGATGCTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
Db 609 GTAGCTACGAGATGCTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 668
QY 541 TCAGTGCATATATGCGCTATTGGTTGTGTTTTCAGAGCTCTGACAGCGCCAGCCACTG 600
Db 669 TCAGTGCATATATGCGCTATTGGTTGTGTTTTCAGAGCTCTGACAGCGCCAGCCACTG 728
QY 601 TGGCTCGAAATCGATGTGGACCAACTTTATCTGATTAATCAGAACACTAG 652
Db 729 TGGCTCGAAATCGATGTGGACCAACTTTATCTGATTAATCAGAACACTAG 780

RESULT 10

US-10-766-691-1
; Sequence 1, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Lex-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-1

Query Match 43.7%; Score 454.4; DB 19; Length 561;
Best Local Similarity 99.8%; Pred. No. 3.6e-110;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGGGTCTTATGGGGTTGTTTCAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGGGTCTTATGGGGTTGTTTCAA 60
QY 61 TGCAGAAACAAACCTCTGGACAGTAGTACGTGTTAAAAATTTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGACAGTAGTACGTGTTAAAAATTTGGAATCTGAAGAT 120
QY 121 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTTGTGAACCTCTCGACAAAGTAGCTGTTAAAAATTTGGAATCTGAAGAT 240
Db 181 CCAATCTTGTGAACCTCTCGACAAAGTAGCTGTTAAAAATTTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGCATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATATACAT 360

Db 181 CCAATCTTGTGAACCTCTCATCGAGTGTTCAGAGAAAGAAAGAAATGCAATTTAGTTTTT 240
QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGCATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATATACAT 360
Db 301 GGAGTGCATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATATACAT 360
QY 361 AACTGTATTTCACAGAGATATAAACTGAAATATTTCTAAATCACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTTCACAGAGATATAAACTGAAATATTTCTAAATCACTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACTTCGGGTTTCACAAATTTCTGATTT 456
Db 421 AAGATTGTGACTTCGGGTTTCACAAATTTCTGATTT 456

RESULT 11

US-10-766-691-7
; Sequence 7, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Lex-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-7

Query Match 43.7%; Score 454.4; DB 19; Length 594;
Best Local Similarity 99.8%; Pred. No. 3.7e-110;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGGGTCTTATGGGGTTGTTTCAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGGGTCTTATGGGGTTGTTTCAA 60
QY 61 TGCAGAAACAAACCTCTGGACAGTAGTACGTGTTAAAAATTTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGACAGTAGTACGTGTTAAAAATTTGGAATCTGAAGAT 120
QY 121 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTTGTGAACCTCTCATCGAGTGTTCAGGAGAAAGAAAGAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCTCATCGAGTGTTCAGGAGAAAGAAAGAAATGCAATTTAGTTTTT 240
QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGCATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATATACAT 360

Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAGCTCTTAATTTCTGTCTATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGAGT 456

RESULT 12

US-09-960-706-1079
; Sequence 1079, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Mungen, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1079
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: (463)..(1539)
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66358
US-09-960-706-1079

Query Match 33.0%; Score 343.8; DB 10; Length 1363;
Best Local Similarity 71.2%; Pred. No. 1.4e-80;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
Qy 1 ATGGAAGATGAAAATTAGTAACTGAGAGAGGCTCTTATGGGTTGTTATTCAAA 60
Db 217 ATGGAGAGATGAAAATAATGGGAAAATTTGGAGAGGATCCTATGAGTTGTTTCAA 276
Qy 61 TGCAGAAACAAAACCTCTGACAGAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
Db 277 TGTAGAAACAGGACACGGGTGAGTTGTGCCATCAAGAGTTTCTGGATCAGAGAT 336
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAAT 180
Db 337 GACCTGTCTATAAGAAAATTTGCCCTTCGGGAAATCCGAATGCTCAAGCAACTCAAGCAT 396
Qy 181 CCAATCTGTGAACCTCATCGAGGTTTTCAGGAGAAAAGGAAAATGCAATTTAGTTTTT 240
Db 397 CCCAACCTTGTAACTCTCGGAGTCTTCAGGAGAAACGGAGGCTTCACCTGGTGT 456
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 457 GAATTTGTGACCAACAGTTTCTCCATGAGTTGAGAGATACCAAGAGGGGTACCGAA 516
Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Db 517 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTCCATATAACAC 576
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 577 AATTTGCATACATAGACAGCTGAAGCCAGAAAATATCTCTATCAGAAACATTCGGTGATT 636
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGAGATGCTTACACCGAT 477
Db 637 AAGCTTTGTGACTTTGGATTGCTCGGCTTTTGCTGGACCGAGTGAATCTACTATACAGAC 696

Qy 478 TATGTAGCTACGAGATGGTACCGAGCTCCCTGAACCTTCTTGTGGAGATACCTCAGTATGGT 537
Db 697 TAGCTGGCTACCGAGTGGTACCGCTCCCTCGAGCTGCTGTGGTGGGACACGCGAGTACGGC 756
Qy 538 TCTTTCACTGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCTCTGACAGGCCAGCCA 597
Db 757 CCCCCGGTGGATGTTTGGGCAATTTGGCTGTCTTCTTGTCTGAGCTGTCTGTCAGGAGTGCCT 816
Qy 598 CTGTGCGCTGGAAAATCAGATGTGGACCAACTTTATCTGTATATCAGAAACACTAGTAGA 656
Db 817 CTGTGGCCAGAAAATCGGATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGGA 875

RESULT 13

US-10-363-616-146
; Sequence 146, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 146
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (463)..(1539)
US-10-363-616-146

Query Match 33.0%; Score 343.8; DB 17; Length 1612;
Best Local Similarity 71.2%; Pred. No. 1.5e-80;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
Qy 1 ATGGAAGATGAAAATTAGTAACTGAGAGAGGCTCTTATGGGTTGTTATTCAAA 60
Db 466 ATGGAGAGATGAAAATAATTTGGGAAAATTTGGAGAGGATCCTATGAGTTGTTTCAA 525
Qy 61 TGCAGAAACAAAACCTCTGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
Db 526 TGTAGAAACAGGACACGGGTGAGTTGTGCCATCAAGAAGTTTCTGGAAATCAGAGAT 585
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAAT 180
Db 586 GACCTGTCTATAAGAAAATTTGCCCTTCGGGAAATCCGAATGCTCAAGCAACTCAAGCAT 645
Qy 181 CCAATCTGTGAACCTCATCGAGGTTTTCAGGAGAAAAGGAAAATGCAATTTAGTTTTT 240
Db 646 CCCAACCTTGTAACTCTCGGAGTCTTCAGAGGAAACGGAGGCTTCACCTGGTGT 705
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 706 GAATTTGTGACCAACAGTTTCTCCATGAGTTGGACAGATACCAAGAGGGGTACAGAA 765
Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Db 766 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTCCCATATAACAC 825
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAAATTTCTAATACTAAGCAAGGAATAATC 420
Db 826 AATTTGCATACATAGACAGCTGAAGCCAGAAAATATCTCTATCAGAAACATTCGGTGATT 885
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGAGATGCTTACACCGAT 477
Db 886 AAGCTTTGTGACTTTGGATTGCTCGGCTTTTGCTGGACCGAGTGAATCTACTATACAGAC 945
Qy 478 TATGTAGCTACGAGATGGTACCGAGCTCCCTGAACCTTCTTGTGGAGATACCTCAGTATGGT 537

Db 946 TAGTGGCTACACAGGTGGTACCGCTCCCTGAGCTGCTGGGGGACACGAGTACGGC 1005
 QY 538 TCTTCAGTCGATATATGGCTATTGGTTGGTTTGGAGAGCTCCTGACGGCCAGCCA 597
 Db 1006 CCCCCTGGTGGATGGTTGGGCAATTGGCTGTGCTTTGGTGGAGTCTGTACGAGTGGCT 1065
 QY 598 CTGTGGCTTGGAAATCAGATGAGACCACTTTATCTGATAATCAGAACACTAGTAGA 656
 Db 1066 CTGTGGCCAGGAAATCGATGCTGATCAGCTGTAICTGATTTAGGAAGACCTTGGGGGA 1124

RESULT 14
 US-10-357-930-24573
 ; Sequence 24573, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24573
 ; LENGTH: 2944
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1, 2, 3, 2940, 2941, 2942, 2943, 2944
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-24573

Query Match 33.0%; Score 343.8; DB 18; Length 2944;
 Best Local Similarity 71.2%; Pred. No. 2.1e-80;
 Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
 QY 1 ATGGAAGAATGATCAAAATAGCTAGACTGAGAGAGGCTCTATGGGTTGTTATTCAAA 60
 Db 829 ATGAGAGATGATGAAAATTTGGGAAATTTGGAGAGGATCTCTATGGAGTTGTTTCAA 888
 QY 61 TGCAGAAACAAACCTCTCGACAAAGTAGTGTGTTTAAATAATTTGTGGAATCTGAAGAT 120
 Db 889 TGTAGAAACAGGACACCGGTGATGTTGGCCATCAAGAGTTCTTGAATCAGAAGAT 948
 QY 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
 Db 949 GACCCCTGTCTAAGAGAAATTTGCCCTTCGGGAAATCCGAATGCTCAAGCACTCAAGCAT 1008
 QY 181 CCAAAATCTTGCAACTCATCAGGTTGTTTCAGAGAGAAAGGAAATGCATTTAGTTTTT 240
 Db 1009 CCAACCTTGTAACTCTGAGAGTCTTCAGAGAGAAACGAGGCTTCACCTGGTGT 1068
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTCAT 300

Db 1069 GAATATTGTGACACACAGTTTCTCCATGAGTTGGACAGATACCAAGAGGGGTACCAGAA 1128
 QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
 Db 1129 CATCTCTGAGAGACATAACTTGGACACACTGCAAGCTGTAAATTTTGGCCATAAACAC 1188
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
 Db 1189 AATTGCATACATAGACAGCTGAAGCCAGAAATATCTCATCAAGAAACATTCGCTGATT 1248
 QY 421 AAGATTGTGACTTCGGTTTGCACAAATTTCTGATT---CCAGAGATGCTTACCCGAT 477
 Db 1249 AAGCTTTGTGACTTTGGATTGTCTCGGCTTTTGACTGGACCGAGTACTACTATACAGAC 1308
 QY 478 TATGTAGCTACGAGATGGTACCGAGCTCTCTGAACTTCTTGTGGAGATATCTCAGTATGGT 537
 Db 1309 TACGTGGCTACCAAGTGGTACCCGCTCCCTGAGCTGCTGTTGGGGACACCGCAGTACGGC 1368
 QY 538 TCTTCAGTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCCTGACAGCCAGCCA 597
 Db 1369 CCCCCGGTGGATGTTTGGGCAATTGGCTGTGCTTGTCTGAGCTGCTGTCAAGAGTGCCT 1428
 QY 598 CTGTGGCTGGAAATCAGATGTGACCAACTTTATCTGATATCAGAACACTAGTAGA 656
 Db 1429 CTGTGGCCAGGAAATCGATGTTGATCAGTGTATCTGATTAGGAAGACCTTGGGGGA 1487

RESULT 15
 US-10-174-794-5
 ; Sequence 5, Application US/10174794
 ; Publication No. US20030166220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/10/174,794
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US/09/411,628
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: US 60/102,906
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1701
 ; TYPE: DNA
 ; ORGANISM: Orcyctolagus cuniculus
 US-10-174-794-5

Query Match 24.2%; Score 251.8; DB 16; Length 1701;
 Best Local Similarity 62.9%; Pred. No. 4.4e-56;
 Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
 QY 1 ATGGAAGAATGATCAAAATAGCTAAGACTGAGAGAGGCTCTATGGGTTGTTATTCAAA 60
 Db 1 ATGGAAGAATGATCAAAATAGCTTGGATTGTTTGGAGAGGAGCTTATGGAATGCTGATGA 60
 QY 61 TGCAGAAACAAACCTCTGGAACAAGTAGTCTGTTTAAATAATTTGTGGAATCTGAAGAT 120
 Db 61 TGTAGGAATAAAGATAGTGGAAAGAAATTTGTGCCATCAAGAGTTCTTAGAAGTGTATGAT 120
 QY 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
 Db 121 GACAAATGGTTTAAATAATGCTATCGGAAATCAAGTTACTAAAGCACTGAGGCAT 180
 QY 181 CCAAAATCTTGGAACCTCATCAGAGTGTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
 Db 181 GAAAAATTTGGTGAATCTCTTGGAGGTGTGTAAAAAAGAAAAAAGCAATGCTACCTAGTCTTT 240
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTCAT 300
 Db 241 GAATTTGTTGACCAACAGATCTTTGATGACTTTTCCAAATGGAAGTATGATGAC 300

Qy	301	GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
Db	301	CAAGTAGTTCAAAAGTATTTGTTTCAGATTATTAATGGAATTGGATTTTGTACAGTCAC	360
Qy	361	AACGTGATTTCACAGAGATATAAACCTGAAATATTCTAATAACTAAGCAGGAATAATC	420
Db	361	AATATCATACATAGAGATATAAGCCAGAGAAATATTTGGTCTCCAGCTGGCGTTGTC	420
Qy	421	AAGATTTTGTGACTTCGGGTTTGCACAAATTCTG---ATTCCAGGAGATGCCCTACACCGAT	477
Db	421	AAGTTATGTGATTTTGGATTTGACGCGACACTGGCAGCTCCCGGAGAGTTTACACTGAT	480
Qy	478	TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGT	537
Db	481	TATGTGCAACTCGATGGTACAGAGCTCCAGAACTACTGTTGGTGTGATGTCAGTATGGC	540
Qy	538	TCTTCAGTCGATATATGGGTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCA	597
Db	541	AAAGCTGTGGATGTGGGCCATTGGTTGTCTGGTAACTGAAATGCTCATGGGGGAACCC	600
Qy	598	CTGTGGCTGGAAATCAGATGTGGACCAACTTTATCTGTATAATCAG	644
Db	601	CTGTTTCTCGAGACTCTGATATTGATCAGCTTTATCTTATTATGAG	647

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OM nucleic - nucleic search, using sw model

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Title: US-10-766-691-9
Perfect score: 1041
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1041	100.0	1041	US-09-671-050-9	Sequence 9, Appli
2	1025	98.5	1068	US-09-671-050-3	Sequence 3, Appli
3	839	80.6	945	US-09-671-050-11	Sequence 11, Appl
4	823	79.1	972	US-09-671-050-5	Sequence 5, Appli
5	709	68.1	1819	US-09-671-050-13	Sequence 13, Appl
6	454.4	43.7	561	US-09-671-050-1	Sequence 1, Appli
7	434.4	43.7	594	US-09-671-050-7	Sequence 7, Appli
8	343.8	33.0	1177	US-09-949-016-1681	Sequence 1681, Ap
9	251.8	24.2	1701	US-09-411-628-5	Sequence 5, Appli
10	251.8	24.2	1701	US-10-174-794-5	Sequence 5, Appli
11	251.8	24.2	3080	US-09-411-628-3	Sequence 3, Appli
12	251.8	24.2	3080	US-10-174-794-3	Sequence 3, Appli
13	241.2	23.2	1794	US-09-949-016-2083	Sequence 2083, Ap
14	163.8	15.7	903	US-08-874-347-9	Sequence 9, Appli
15	163.8	15.7	903	US-09-093-522-9	Sequence 9, Appli
16	162	15.6	1476	US-09-969-106-1	Sequence 1, Appli
17	162	15.6	1476	US-09-338-125-1	Sequence 1, Appli
18	162	15.6	1476	US-09-266-225D-13	Sequence 13, Appl
19	162	15.6	1635	US-09-417-197-112	Sequence 112, App
20	162	15.6	1635	US-09-417-197-114	Sequence 114, App
21	160.4	15.4	1296	US-09-949-016-2154	Sequence 2154, Ap
22	160.4	15.4	2213	US-09-023-655-1037	Sequence 1037, Ap
23	154.2	14.8	1050	US-09-220-132-3	Sequence 3, Appli
24	154.2	14.8	1825	US-09-949-039-115	Sequence 115, App
25	151	14.5	1042	US-09-949-016-4802	Sequence 4802, Ap
26	145.8	14.0	3823	US-09-949-016-4276	Sequence 4276, Ap
27	134.8	12.9	1158	US-09-949-016-4906	Sequence 4906, Ap

28	134.8	12.9	1161	4	US-09-023-655-1373	Sequence 1373, Ap
29	134.8	12.9	1161	4	US-09-949-016-181	Sequence 181, App
30	134.8	12.9	1825	4	US-09-620-312B-313	Sequence 313, App
31	133.2	12.8	987	4	US-09-949-016-5854	Sequence 5854, Ap
32	133.2	12.8	1089	1	US-08-154-915-1	Sequence 1, Appli
33	133.2	12.8	1089	2	US-08-464-517-37	Sequence 37, Appl
34	133.2	12.8	1089	2	US-08-246-361A-37	Sequence 37, Appl
35	133.2	12.8	1089	3	US-08-463-772-37	Sequence 37, Appl
36	133.2	12.8	1089	5	PCT-US93-09945-1	Sequence 1, Appli
37	128	12.3	993	4	US-09-248-796A-4323	Sequence 4323, Ap
38	128	12.3	1002	1	US-08-463-090B-3	Sequence 3, Appli
39	119.2	11.5	1044	4	US-09-248-796A-4325	Sequence 4325, Ap
40	116	11.1	1070	1	US-08-463-090B-5	Sequence 5, Appli
41	113.2	10.9	69909	4	US-09-949-016-13423	Sequence 13423, A
42	112	10.8	1308	4	US-09-801-861-4	Sequence 4, Appli
43	112	10.8	1308	4	US-10-224-562-4	Sequence 4, Appli
44	112	10.8	2203	4	US-09-801-861-1	Sequence 1, Appli
45	112	10.8	2203	4	US-10-224-562-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-671-050-9
; Sequence 9, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-9

Query Match	100.0%;	Score 1041;	DB 4;	Length 1041;
Best Local Similarity	100.0%;	Pred. No. 1.7e-285;		
Matches 1041;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	ATGAAAAGTATGAAAAATAGCTAGACCTGGAGAGGGCTTATGGGTTGTTATTCAAA	60	
Db	1	ATGAAAAGTATGAAAAATAGCTAGACCTGGAGAGGGCTTATGGGTTGTTATTCAAA	60	
Qy	61	TGAGAAACAAAACCTCTGACAAAGTAGTAGCTTTAAAAAATTTGTGGAATCTGAAGAT	120	
Db	61	TGAGAAACAAAACCTCTGACAAAGTAGTAGCTTTAAAAAATTTGTGGAATCTGAAGAT	120	
Qy	121	GATCCTGTTCTTAAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAAGCAATTAACAT	180	
Db	121	GATCCTGTTCTTAAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAAGCAATTAACAT	180	
Qy	181	CCAAATCTTGTGAACCTCATCGAGGTTTCAGAGAAAAGAAAATGCAATTTAGTTTTT	240	
Db	181	CCAAATCTTGTGAACCTCATCGAGGTTTCAGAGAAAAGAAAATGCAATTTAGTTTTT	240	
Qy	241	GAATACCTGTCATCATACACATTTTAAATGAGCTGAGAAAGAACCCAAATGGAGTTGCTGAT	300	
Db	241	GAATACCTGTCATCATACACATTTTAAATGAGCTGAGAAAGAACCCAAATGGAGTTGCTGAT	300	

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QY 301 GGAGTGATCAAAACGGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAACGGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATATC 420
QY 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGAGATGCTTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGAGATGCTTACACCGATTAT 480
QY 481 GTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
QY 541 TCAGTCCATATATGGGCTATTGGTGTGTTTTCAGAGCTCTGACAGGCCAGCCACTG 600
Db 541 TCAGTCCATATATGGGCTATTGGTGTGTTTTCAGAGCTCTGACAGGCCAGCCACTG 600
QY 601 TGGCTCGAAATCAGATGTGGACCAACTTATCTGATAATCAGAACACTAGTAGAGACG 660
Db 601 TGGCTCGAAATCAGATGTGGACCAACTTATCTGATAATCAGAACACTAGTAGAGACG 660
QY 661 GGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
QY 721 GTAGCTCTCAAGTGTGAAATACAGGAATTAATCCAGACATCAATCAATCTTT 780
Db 721 GTAGCTCTCAAGTGTGAAATACAGGAATTAATCCAGACATCAATCAATCTTT 780
QY 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 840
Db 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 840
QY 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTCAAGAGGGGTGTCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTCAAGAGGGGTGTCTGAAG 900
QY 901 ATGAATCCAGATGACAGATTAAGCTGTTCGCAACTCTCGAGAGCTCTCTACTTTGATTCT 960
Db 901 ATGAATCCAGATGACAGATTAAGCTGTTCGCAACTCTCGAGAGCTCTCTACTTTGATTCT 960
QY 1021 CAGGTACTTCCGCTCAAAAGT 1041
Db 1021 CAGGTACTTCCGCTCAAAAGT 1041

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RESULT 2

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US-09-671-050-3
; Sequence 3, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/671.050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-671-050-3

Query Match      98.5%; Score 1025; DB 4; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9e-281;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGAATGATGAAAAATAGCTAGACCTGAGAGAGGGCTCTTATGGGGTGTATTTCAAA 60
Db 1 ATGGAAGAATGATGAAAAATAGCTAGACCTGAGAGAGGGCTCTTATGGGGTGTATTTCAAA 60
QY 61 TGCAGAAAAACAAACCTCTGACCAAGTAGTAGCTGTTAAAAAATTTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAAAACAAACCTCTGACCAAGTAGTAGCTGTTAAAAAATTTTGGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAATAAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAATAAT 180
QY 181 CCAATCTGTTGAACCTCATCGAGGTGTTCCAGAGAAAAAGGAAAAATGCAATTTAGTTTT 240
Db 181 CCAATCTGTTGAACCTCATCGAGGTGTTCCAGAGAAAAAGGAAAAATGCAATTTAGTTTT 240
QY 241 GAATCTGTCATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
Db 241 GAATCTGTCATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGSCAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGSCAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
QY 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTTAATACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTTAATACTAAGCAAGGAATATC 420
QY 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATTTCCAGAGATGCTTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATTTCCAGAGATGCTTACACCGATTAT 480
QY 481 GTAGTACGAGATGTAACCGAGCTCTCGAACTTCTTGTGGGAGATACCTCAGTATGTTCT 540
Db 481 GTAGTACGAGATGTAACCGAGCTCTCGAACTTCTTGTGGGAGATACCTCAGTATGTTCT 540
QY 541 TCAGTCCATATATGGGCTATTGGTGTGTTTTCAGAGCTCTGACAGGCCAGCCACTG 600
Db 541 TCAGTCCATATATGGGCTATTGGTGTGTTTTCAGAGCTCTGACAGGCCAGCCACTG 600
QY 601 TGGCTCGAAATCAGATGTGGACCAACTTATCTGATAATCAGAACACTAGTAGAGACG 660
Db 601 TGGCTCGAAATCAGATGTGGACCAACTTATCTGATAATCAGAACACTAGTAGAGACG 660
QY 661 GGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
QY 721 GTAGCTCTCAAGTGTGAAATACAGGAATTAATCCAGACATCAATCAATCTTT 780
Db 721 GTAGCTCTCAAGTGTGAAATACAGGAATTAATCCAGACATCAATCAATCTTT 780
QY 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 840
Db 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 840
QY 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTCAAGAGGGGTGTCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTCAAGAGGGGTGTCTGAAG 900
QY 901 ATGAATCCAGATGACAGATTAAGCTGTTCGCAACTCTCGAGAGCTCTCTACTTTGATTCT 960
Db 901 ATGAATCCAGATGACAGATTAAGCTGTTCGCAACTCTCGAGAGCTCTCTACTTTGATTCT 960

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Qy 961 TTTCAAGAGGCCCAATTAAGAAAGCACTGTAATGAAGAAAGCAAGAAAGAGCGCAA 1020
 Db 961 TTTCAAGAGGCCCAATTAAGAAAGCACTGTAATGAAGAAAGCAAGAAAGAGCGCAA 1020
 Qy 1021 CAGGT 1025
 Db 1021 CAGGT 1025
 RESULT 3
 US-09-671-050-11
 ; Sequence 11, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 945
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-671-050-11

Query Match 80.6%; Score 839; DB 4; Length 945;
 Best Local Similarity 90.8%; Pred. No. 3.5e-228;
 Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 Qy 1 ATGGAAGAGTATGAAATTAAGTAAAGCTGAGAGGGTCTTATGGGTTGTATTCAA 60
 Db 1 ATGGAAGAGTATGAAATTAAGTAAAGCTGAGAGGGTCTTATGGGTTGTATTCAA 60
 Qy 61 TGCAGAAACAAACCTCTGACAAAGTAGTCTGTAAAAAATTTGTGGAATCTGAAGAT 120
 Db 61 TGCAGAAACAAACCTCTGACAAAGTAGTCTGTAAAAAATTTGTGGAATCTGAAGAT 120
 Qy 121 GATCTGTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
 Db 121 GATCTGTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
 Qy 181 CCAATCTGTGAACTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTT 240
 Db 181 CCAATCTGTGAACTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTT 240
 Qy 241 GAATACCTGTATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTGTCTGAT 300
 Db 241 GAATACCTGTATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTGTCTGAT 300
 Qy 301 GGAGTGATCAAAAGGTTATTTAGCAAAACACTTCAGCTCTTAATTTCTGTATATACAT 360
 Db 301 GGAGTGATCAAAAGGTTATTTAGCAAAACACTTCAGCTCTTAATTTCTGTATATACAT 360
 Qy 361 AACTGTATTCAGAGATATAAACCTGAAATTTCTTAATTAACCTAAGCAAGGATATATC 420
 Db 361 AACTGTATTCAGAGATATAAACCTGAAATTTCTTAATTAACCTAAGCAAGGATATATC 420
 Qy 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGGAGATGCCCTACACCGATTAT 480
 Db 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGGAGATGCCCTACACCGATTAT 480
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTCTGTGGAGATACCTCAGTATGGTTCT 540

Db 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGAGATACCTCAGTATGGTTCT 540
 Qy 541 TCACTCGATATATGGGCTATTTGGTGTGTTTTTTCAGAGCTCTCTGACAGCCAGCCACTG 600
 Db 541 TCACTCGATATATGGGCTATTTGGTGTGTTTTTTCAGAGCTCTCTGACAGCCAGCCACTG 600
 Qy 601 TGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATATCAGAACACTAGTAGAGACG 660
 Db 601 TGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATATCAGAACACTAGTAGAGACG 660
 Qy 661 GGGTTTCGCCCATGTTGACCCAGGCTGGTCTCGAACTTCTTACGTCAAGTGATCCACCTGCC 720
 Db 661 GGGTTTCGCCCATGTTGACCCAGGCTGGTCTCGAACTTCTTACGTCAAGTGATCCACCTGCC 720
 Qy 721 GTAGCCTCTCAAAGTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
 Db 721 GTAGCCTCTCAAAGTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
 Qy 781 AAAAGTAAACGGTTTTTCCATGCGATCAGTATACCTGAGCCAGGAGACATGGAACCTCTT 840
 Db 781 AAAAGTAAACGGTTTTTCCATGCGATCAGTATACCTGAGCCAGGAGACATGGAACCTCTT 840
 Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAAAGGGGTGCTGAAG 900
 Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAAAGGGGTGCTGAAG 900
 Qy 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTTCTTTGATTCT 960
 Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTTCTTTGATTCT 960
 Qy 961 TTTCAAGAGGCCCAATTAAGAAAGCACTGTAATGAAGAAAGCAAGAAAGAGCGCAA 1020
 Db 961 TTTCAAGAGGCCCAATTAAGAAAGCACTGTAATGAAGAAAGCAAGAAAGAGCGCAA 1020
 Qy 1021 CAGGTACTTCGGCTCAAAAGT 1041
 Db 925 CAGGTACTTCGGCTCAAAAGT 945

RESULT 4
 US-09-671-050-5
 ; Sequence 5, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 972
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-671-050-5

Query Match 79.1%; Score 823; DB 4; Length 972;
 Best Local Similarity 90.6%; Pred. No. 1.2e-223;
 Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 Qy 1 ATGGAAGATGATGAAATTAAGCTTAAGCTGAGAGGGTCTTATGGGTTGTATTCAA 60
 Db 1 ATGGAAGATGATGAAATTAAGCTTAAGCTGAGAGGGTCTTATGGGTTGTATTCAA 60

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QY 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTCAAGAT 120
Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTCAAGAT 120
QY 121 GATCCTGTTGTTAAGAAATACGACTAAGAGAAATACGATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTTGTTAAGAAATACGACTAAGAGAAATACGATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTGTGATCATACACTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 240
Db 181 CCAATCTGTGATCATACACTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 240
QY 241 GAATCTGTGATCATACACTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 300
Db 241 GAATCTGTGATCATACACTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 360
QY 361 AACTGTATTACAGAGATATAAACCCTGAAATATTCTAATACTAAGCAAGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAACCCTGAAATATTCTAATACTAAGCAAGAAATATC 420
QY 421 AAGATTTGCTGCTCGGTTTGCACAACTTCAAGCTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 480
Db 421 AAGATTTGCTGCTCGGTTTGCACAACTTCAAGCTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 480
QY 481 GTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATCACTAGTATGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATCACTAGTATGTTCT 540
QY 541 TCAGTTCGATATATGGCTATATGGCTATATGGCTATATGGCTATATGGCTATATGGCT 600
Db 541 TCAGTTCGATATATGGCTATATGGCTATATGGCTATATGGCTATATGGCTATATGGCT 600
QY 601 TGCCCTGGAATATCAGATGTGACCAACTTTATCTGTGATATCAGAACACTAGTAGAGAG 660
Db 601 TGCCCTGGAATATCAGATGTGACCAACTTTATCTGTGATATCAGAACACTAGTAGAGAG 660
QY 661 GGGTTTCGCCATGTTGACAGAGCTGGTCTCGAACTCTTGAAGTCAAGTATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTTGACAGAGCTGGTCTCGAACTCTTGAAGTCAAGTATCCACCTGCC 720
QY 721 GTAGCCTCTCAAGTGTGGAATATCAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCCTCTCAAGTGTGGAATATCAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
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Db 781 AAAAGTAAACGGTTTTCATGCGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
QY 841 GAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCAATGAGGGGTGCTGAAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCAATGAGGGGTGCTGAAAG 900
QY 901 ATGAATCCAGATGACAGATTAACCTGTTCCTCAACTCTCTGAGAGCTTCACTTTGATCT 960
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCTCAACTCTCTGAGAGCTTCACTTTGATCT 960
QY 961 TTTCAAGAGCCCAATTAAGAAAGCAAGCAAGTAAATGAAGAGGAAACAGAGAGCCCAA 1020
Db 961 TTTCAAGAGCCCAATTAAGAAAGCAAGCAAGTAAATGAAGAGGAAACAGAGAGCCCAA 1020
QY 1021 CAGGT 1025
Db 925 CAGGT 929

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RESULT 5
US-09-671-050-13
Sequence 13, Application US/09671050

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; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671.050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-671-050-13

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Query Match
Best Local Similarity 68.1%; Score 709; DB 4; Length 1819;
Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

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QY 1 ATGCAAAAGTATGCAAAATTTAGCTAAGACTGAGAGAGGCTCTTATGGGGTGTATTCAAA 60
Db 138 ATGCAAAAGTATGCAAAATTTAGCTAAGACTGAGAGAGGCTCTTATGGGGTGTATTCAAA 197
QY 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTCAAGAT 120
Db 198 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTCAAGAT 257
QY 121 GATCCTGTTGTTAAGAAATACGACTAAGAGAAATACGATGTTGAAGCAATTAACAT 180
Db 258 GATCCTGTTGTTAAGAAATACGACTAAGAGAAATACGATGTTGAAGCAATTAACAT 317
QY 181 CCAATCTGTGAACTCTCATCGAGGTGTTCAAGAGAAAGGAAATGCAATTTAGTTTTT 240
Db 318 CCAATCTGTGAACTCTCATCGAGGTGTTCAAGAGAAAGGAAATGCAATTTAGTTTTT 377
QY 241 GAATCTCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 300
Db 378 GAATCTCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGGTGCTGAT 437
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 438 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 497
QY 361 AACTGTATTCACAGAGATATAAACCCTGAAATATTCTAATACTAAGCAAGAAATATC 420
Db 498 AACTGTATTCACAGAGATATAAACCCTGAAATATTCTAATACTAAGCAAGAAATATC 557
QY 421 AAGATTTGCTGACTTCGGGTTTGCACAAATTTCTG- 453
Db 558 AAGATTTGCTGACTTCGGGTTTGCACAAATTTCTGAGTTGAGCTTCATCTTCTCTGCTGCC 617
QY 454 ----- 453
Db 618 TCCTTGATTTGCTTAATAGTTGACCTTCTGAATTTCTTTTCTGCCAATTCAGAGATTTT 677
QY 454 ----- 453
Db 678 CTCTTGCTTTGATCCATTTGCTGACACAGTGTTCACCATGGGGCCAGGCTCATCTCGA 737
QY 454 ----- 453
Db 738 ACTTCTGGCTCAAGTGTATCTTCCACCTCGGCTTCCCAAGTGTGATTCGAAGTGTG 797
QY 454 ----- 453

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Db 798 AGCCACGTCGCCAGCCAGATTTTCAACAATACTACTGAGAGCTCAACAAGATTGTTT 857
Qy 454 -----ATTCCAGGAGATGCTACACC 474
Db 858 TTAGTGGGAACAACAATTCGAACAAATTCCTTGAGAACGCATTCAGGAGATGCTACACC 917
Qy 475 GATTATGCTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTGTGGGAGATATCTCAGTAT 534
Db 918 GATTATGCTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTGTGGGAGATATCTCAGTAT 977
Qy 535 GGTTCCTCAGTCGATATATGGGCTATTGGTGTGTTTTTTCGAGAGCTCCTGACAGGCCAG 594
Db 978 GGTTCCTCAGTCGATATATGGGCTATTGGTGTGTTTTTTCGAGAGCTCCTGACAGGCCAG 1037
Qy 595 CCACTGTGGCTGGAAATCAGATGTGGACCAACTTTTATCTGATAATCAAGAACACTAGTA 654
Db 1038 CCACTGTGGCTGGAAATCAGATGTGGACCAACTTTTATCTGATAATCAAGAACACTAGTA 1097
Qy 655 GAGACGGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGAGCTCAAGTGATCCA 714
Db 1098 GAGACGGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGAGCTCAAGTGATCCA 1157
Qy 715 CCTGCCGTAGCCTCTCAAGTGTGGAAATACAGGAAATTAATCCCAAGACATCAATCA 774
Db 1158 CCTGCCGTAGCCTCTCAAGTGTGGAAATTAATCCCAAGACATCAATCA 1217
Qy 775 ATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 834
Db 1218 ATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 1277
Qy 835 ACTCTTGAGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCATGAAGGGGTGT 894
Db 1278 ACTCTTGAGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCATGAAGGGGTGT 1337
Qy 895 CTGAAGATGAATCCAGATGACAGATTAACTCTGTTCCCACTCTCTGGAGAGCTCTACTTT 954
Db 1338 CTGAAGATGAATCCAGATGACAGATTAACTCTGTTCCCACTCTCTGGAGAGCTCTACTTT 1397
Qy 955 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAGACAGTAAATGAAGGAAGAAACAGAGA 1014
Db 1398 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAGACAGTAAATGAAGGAAGAAACAGAGA 1457
Qy 1015 CGCCAACAGGT 1025
Db 1458 CGCCAACAGGT 1468

RESULT 6
US-09-671-050-1
; Sequence 1, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US/09/671.050
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-1

Query Match 43.7%; Score 454.4; DB 4; Length 561;
Best Local Similarity 99.8%; Pred. No. 4.1e-119;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Qy 61 TGCAGAAAAACCAACCTCTGGAACAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAAAACCAACCTCTGGAACAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 180
Qy 181 CCAAACTCTTGTAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAAACTCTTGTAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATACGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATACGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Qy 301 GAGTGTATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 301 GAGTGTATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACTGAAATATTCTAATAACTAAGCAAGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACTGAAATATTCTAATAACTAAGCAAGAAATATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGATT 456
Db 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGATT 456
RESULT 7
US-09-671-050-7
; Sequence 7, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US/09/671.050
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-7
Query Match 43.7%; Score 454.4; DB 4; Length 594;
Best Local Similarity 99.8%; Pred. No. 4.2e-119;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Qy 61 TGCAGAAAAACCAACCTCTGGAACAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAAAACCAACCTCTGGAACAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120

Db 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
QY 181 CCAAAATCTTGTAACCTCATCGAGGTGTTCCAGAGAGAAAAGGAAAATGCAATTTAGTTTTT 240
Db 181 CCAAAATCTTGTAACCTCATCGAGGTGTTCCAGAGAGAAAAGGAAAATGCAATTTAGTTTTT 240
QY 241 GATATCTGTCATCATACACTTTTAAATAGCTGGAAGAAACCCAAATCGAGTTCGTGAT 300
Db 241 GATATCTGTCATCATACACTTTTAAATAGCTGGAAGAAACCCAAATCGAGTTCGTGAT 300
QY 301 GGAGTATCAAAAGCGTATATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 301 GGAGTATCAAAAGCGTATATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
QY 361 AACTGTATTACAGAGATATAAACCTGAAATATTTCTAATAACTAAGCAAGGATTAATC 420
Db 361 AACTGTATTACAGAGATATAAACCTGAAATATTTCTAATAACTAAGCAAGGATTAATC 420
QY 421 AAGATTGTCAGCTTCGGGTTTCACAAATTCGTATT 456
Db 421 AAGATTGTCAGCTTCGGGTTTCACAAATTCGTATT 456

RESULT 8

US-09-949-016-1681
; Sequence 1681, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1681
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1681

Query Match 33.0%; Score 343.8; DB 4; Length 1177;
Best Local Similarity 71.2%; Pred. No. 1.5e-87;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
QY 1 ATGGAAGAATGATGAAAAATTTAGCTAAGCTGAGAGAGGCTCTATGGGGTTGTTATTCAAA 60
Db 32 ATGGAAGAATGATGAAAAATTTGGAATTTGGAGAGGATCTATGGAGTTGTTTTCAAA 91
QY 61 TGCAGAAACAAACCTCTCGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 92 TGTAGAAACAGGACACCGGTCAGATTGTGGCCATCAAGAAGTTCTTGGAAATCAGAAGAT 151
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db 152 GACCCCTGTCATAGAAATTTGCCCTTCGGAAATCCGAATGCTCAAGCAACTCAAGCAT 211
QY 181 CCAAAATCTTGTAACCTCATCGAGGTGTTCCAGAGAGAAAAGGAAAATGCAATTTAGTTTTT 240
Db 212 CCAAAATCTTGTAACCTCATCGAGGTGTTCCAGAGAGAAAAGGAAAATGCAATTTAGTTTTT 271
QY 241 GAATATCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCCAAATGGAGTTGTCGAT 300

Db 272 GAATATCTGTGACCAACACAGTTCTCCATGAGTTGCACAGATACCAAAAGGGGTACAGAA 331
QY 301 GGAGTATCAAAAGCGTATATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 332 CATCTCGTGAAGACATAAATGCGCAGCACTGCAAGCTGTAATTTTCCCAATAACAC 391
QY 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTAATAACTAAGCAAGCAATTAATC 420
Db 392 AATTCATATACATAGAGACGTAAGCCAGAAATATCTCATCAGAAACATTCCTGATTT 451
QY 421 AAGATTGTCAGCTTCGGGTTTCACAAATTCGTATT---CCAGAGATGCTTACACCGAT 477
Db 452 AAGCTTTGTCAGCTTTGCAATTTGCTCGGCTTTTACTGGACCGAGTGACTACTATACAGAC 511
QY 478 TATGTAGTACAGAGATGTTACCGAGCTCTCGAACTTTCTGTGGGAGATCTCAGTATGCT 537
Db 512 TAGCTGCTACCAAGTGTGTACCGCTCCCTGAGCTCTGCTGGGGACACGCAAGTACGCG 571
QY 538 TCTTTCAGTGCATATATGGGCTATTTGCTGTTTGTGAGAGCTCTCTGACAGCCAGCCCA 597
Db 572 CCCCCGTTGAGTGTGGGCAATTTGGCTGTCTTTTGTGAGCTGCTGTCCAGAGTGCCT 631
QY 598 CTGTGCTGGAATAATCAGATGTGGAACCACTTTATCTGATAATCAGAACTACTAGTAGA 656
Db 632 CTGTGCTGGAATAATCAGATGTGGAATGATGATGATGATGATGATGATGATGATGATGAT 690

RESULT 9

US-09-411-628-5
; Sequence 5, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-09-411-628-5

Query Match 24.2%; Score 251.8; DB 3; Length 1701;
Best Local Similarity 62.9%; Pred. No. 2.4e-61;
Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
QY 1 ATGGAAGAATGATGAAAAATTTAGCTAAGCTGAGAGAGGCTCTATGGGGTTGTTATTCAAA 60
Db 1 ATGGAAGAATGATGAAAAATTTGGAATTTGGAGAGGAGTTATGGAATGGTGAAG 60
QY 61 TGCAGAAACAAACCTCTCGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGTAGAAATAGAGATAGTGGAGAAATTTGGCCATCAAGAAGTTCTTGAAGATGATGAT 120
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db 121 GACAAAAATGTTAAAAAATTTCTATGCGAGAAATCAAGTTACTTAAGCAACTGAGGCAT 180
QY 181 CCAAAATCTTGTAACCTCATCGAGGTGTTCCAGAGAGAAAAGGAAAATGCAATTTAGTTTTT 240
Db 181 GAAAAATTTGTTGAATCTGTTGGAGGTGTGTAAAAAAGGAAAACGATGTTACCTAGTCTTT 240
QY 241 GAATATCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCCAAATGGAGTTGTCGAT 300
Db 241 GAATTTGTTGACCAACAGATTTCTGATGACTTGGAACTCTTTTCCAAATGGAGTATGATGAC 300

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Qy 301 GGAGTGATCAAAAGCGTATTATGCGAACACCTTCAAGCTCTTAATTTCTGTCTATACAT 360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 CAAGTAGTTCAAAAGTATTCTTTTTCAGATTAATTAATGAATTTGTTGTCACAGTCAC 360
Qy 361 AACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAGCAAGGAATAATC 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 AATATCATACATAGAGATATAAAGCCAGAGATATATTGGTCTCCAGTCTGGCGTTGTC 420
Qy 421 AAGATTGTGACTTGGGTTTGGCAAAATTCG---ATTCCAGAGATGCCCTACACCGAT 477
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AAGTTATGTGATTTTGGATTTCACGGACACTGGCAGCTCCCGAGAGGTTTACACTGAT 480
Qy 478 TATCTAGCTACGAGATGGTACCGAGCTCTGAACTTTCTTGGGAGATACCTACGATATGGT 537
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 TATGTGCAACTCGATGGTACAGAGCTCCAGAACTACTCTGGTGGTGGATGTCACGATATGGC 540
Qy 538 TCTTCAGTTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTTGCAGAGGCCAGCA 597
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 AAAGCTGTGGATGTGGGCCATTGGTTGCTGCTGTAACCTGAATGCTCATGGGGGAACCC 600
Qy 598 CTGTGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATATACAG 644
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 CTGTTCTCGAGACTCTGATATTGATCAGCTTTATCTTATTATGAG 647

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RESULT 10
US-10-174-794-5
; Sequence 5, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10174,794
; PRIOR FILING DATE: 2002-06-18
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5

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Query Match 24.2%; Score 251.8; DB 4; Length 1701;
Best Local Similarity 62.9%; Pred. No. 2.4e-61;
Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

Qy 1 ATGGAAGAAGTATGAAAAATTAGCTTAAGACTGGAGAGGGTCTTATGGGTTGTATTCAA 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 ATGGAANAATATAGAACCTTGGATTGGTTGGAGAGGGAGTTATGGAATGGTATGAAG 60
Qy 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGAAATCTGAAGAT 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 TGTAGGAATAAAGATAGTGGAGAAATTTGGCCCAATCAAGAAGTTCTTAGAAAGTGATGAT 120
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACACAT 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 GACAAAAATGGTTAAAAAATTTGCTATGCGAGAAATCAAGTTACTTAAAGCAACTGAGGCAT 180
Qy 181 CCAAACTCTGTGAACCTCATCGAGTGTTCAGGAGAAAAAGGAAATATGCAATTTAGTTTTT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 GAAAAATTTGGTGAATCTGTTGGAGGTGTGTAAAAAATAAACAATGGTACCTAGTCTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 GAAATTTGTGACCAACAGATTTCTTGATGACTTGGAACTCTTTCCAAATGGACTAGATGAC 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATACAT 360

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Db 301 CAAGTAGTTCAAAAGTATTGTTTTCAGATTAATTAATGAATTTGTTGTCACAGTCAC 360
Qy 361 AACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAGCAAGGAATAATC 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 AATATCATACATAGAGATATAAAGCCAGAGATATATTGGTCTCCAGTCTGGCGTTGTC 420
Qy 421 AAGATTGTGACTTGGGTTTGGCAAAATTCG---ATTCCAGAGATGCCCTACACCGAT 477
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AAGTTATGTGATTTTGGATTTCACGGACACTGGCAGCTCCCGAGAGGTTTACACTGAT 480
Qy 478 TATCTAGCTACGAGATGGTACCGAGCTCTGAACTTTCTTGGGAGATACCTACGATATGGT 537
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 TATGTGCAACTCGATGGTACAGAGCTCCAGAACTACTCTGGTGGTGGATGTCACGATATGGC 540
Qy 538 TCTTCAGTTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTTGCAGAGGCCAGCA 597
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 AAAGCTGTGGATGTGGGCCATTGGTTGCTGCTGTAACCTGAATGCTCATGGGGGAACCC 600
Qy 598 CTGTGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATATACAG 644
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 CTGTTCTCGAGACTCTGATATTGATCAGCTTTATCTTATTATGAG 647

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RESULT 11
US-09-411-628-3
; Sequence 3, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)...(1949)
US-09-411-628-3

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Query Match 24.2%; Score 251.8; DB 3; Length 3080;
Best Local Similarity 62.9%; Pred. No. 3.2e-61;
Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

Qy 1 ATGGAAGAAGTATGAAAAATTAGCTTAAGACTGGAGAGGGTCTTATGGGTTGTATTCAA 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
249 ATGGAANAATATAGAACCTTGGATTGGTTGGAGAGGGAGTTATGGAATGGTATGAAG 308
Qy 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGAAATCTGAAGAT 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
309 TGTAGGAATAAAGATAGTGGAGAAATTTGGCCCAATCAAGAAGTTCTTAGAAAGTGATGAT 368
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACACAT 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 GACAAAAATGGTTAAAAAATTTGCTATGCGAGAAATCAAGTTACTTAAAGCAACTGAGGCAT 428
Qy 181 CCAAACTCTGTGAACCTCATCGAGTGTTCAGGAGAAAAAGGAAATATGCAATTTAGTTTTT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
429 GAAAAATTTGGTGAATCTGTTGGAGGTGTGTAAAAAATAAACAATGGTACCTAGTCTTTT 488
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
489 GAAATTTGTGACCAACAGATTTCTTGATGACTTGGAACTCTTTCCAAATGGACTAGATGAC 548
Qy 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATACAT 360

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Db 549 CAAGTAGTCAAAAGTATTGTTTCAGATTATTAATGGAATGGAATTTGTACAGTCAC 608
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGAAATAATC 420
Db 609 AATATCATACATAGAGATATAAAGCCAGAGAAATATATGTTCTCCAGTCTGGCGTTGTC 668
Qy 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTG--ATTCCAGGAGATCCCTACACCGAT 477
Db 669 AAGTTATGTGATTTGGAATTTGACCGACACTGGCAGCTCCCGGAGAGTTTACACTGAT 728
Qy 478 TATGTAGCTACAGAGATGTTACCGAGCTCTGAACTTTCTTGTGGGAGATCTCAGTATGTT 537
Db 729 TATGTGGCAACTCGATGGTACAGCTCCAGAACTACTGTTTGGTGAATGCTCAAGTATGCG 788
Qy 538 TCTTCAGTCGATATATGGCTATTTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCA 597
Db 789 AAAGCTGTGATGTTGGGCCATTTGTTCTGGTAACTGAAATGCTCATGGGGAACCC 848
Qy 598 CTGTGGCTCGGAAATCAGATGTGGACCACTTTATCTGATAATCAG 644
Db 849 CTGTTTCTGGAGACTCTGATATTCATCAGCTTTTATCTATTATGAG 895

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RESULT 12

US-10-174-794-3

; Sequence 3, Application US/10174794

; Patent No. 6664086

; GENERAL INFORMATION:

; APPLICANT: University of Southern California

; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN

; FILE REFERENCE: 13761-707

; CURRENT APPLICATION NUMBER: US/10/174,794

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: US/09/411,628

; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/102,906

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 3080

; TYPE: DNA

; ORGANISM: *Oryctolagus cuniculus*

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (249)....(1949)

US-10-174-794-3

Query Match

Best Local Similarity 24.2%; Score 251.8; DB 4; Length 3080;

Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

```

Qy 1 ATCGAAAGTATCAAAAATTAGCTAAGCTGGAGAGGGTCTTATGGGTTGTATTCAA 60
Db 249 ATGGAAAAATATGAGAACCTTGGATTGGTTGGAGAGCGAGTTATGGAATGTTGATGAG 308
Qy 61 TGCAGAAAACAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 309 TGTAGGAATAAGATAGTGGAGAAATTTGGCCATCAAGAGTCTCTAGAAAGTGTATGAT 368
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTTATTTGAAGCAATTTAAACAT 180
Db 369 GACAAAATGGTTAAAAAATTTGCTATGCGAGAAATCAAGTTACTAAGCAACTGAGGAT 428
Qy 181 CCAAAATCTTGTGAACCTCATCGAGTGTTCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 429 GAAAATTTGTTGAATCTGTTGAGGTGTGTAAGAAAAAAGAAAAACGATGTTACCTAGTCTTT 488
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 489 GAAATTTGTTGACACACAGATTCTTGATGACTTTGGAACCTTTTCCAAATGGACTAGATGAC 548

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Qy 301 GGAGTGATCAAAAGCTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 549 CAAGTAGTCAAAAGTATTGTTTCAGATTATTAATGGAATGGAATTTGTACAGTCAC 608
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGAAATAATC 420
Db 609 AATATCATACATAGAGATATAAAGCCAGAGAAATATATGTTCTCCAGTCTGGCGTTGTC 668
Qy 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTG--ATTCCAGGAGATCCCTACACCGAT 477
Db 669 AAGTTATGTGATTTGGAATTTGACCGACACTGGCAGCTCCCGGAGAGTTTACACTGAT 728
Qy 478 TATGTAGCTACAGAGATGTTACCGAGCTCTGAACTTTCTTGTGGGAGATCTCAGTATGTT 537
Db 729 TATGTGGCAACTCGATGGTACAGCTCCAGAACTACTGTTTGGTGAATGCTCAAGTATGCG 788
Qy 538 TCTTCAGTCGATATATGGCTATTTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCA 597
Db 789 AAAGCTGTGATGTTGGGCCATTTGTTCTGGTAACTGAAATGCTCATGGGGAACCC 848
Qy 598 CTGTGGCTCGGAAATCAGATGTGGACCACTTTATCTGATAATCAG 644
Db 849 CTGTTTCTGGAGACTCTGATATTCATCAGCTTTTATCTATTATGAG 895

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RESULT 13

US-09-949-016-2083

; Sequence 2083, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2083

; LENGTH: 1794

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-2083

Query Match

Best Local Similarity 23.2%; Score 241.2; DB 4; Length 1794;

Matches 400; Conservative 0; Mismatches 243; Indels 3; Gaps 1;

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Qy 1 ATGAAAAGTATGAAAAATTAGCTAAGCTGGAGAGGGTCTTATGGGTTGTATTCAA 60
Db 376 ATGGAAAAATATGAAAAACCTGGGTTTGGTGGAGAGGGAGTTATGGAATGTTGATGAAG 435
Qy 61 TGCAGAAAACAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 436 TGTAGGAATAAGATAGTGGAGAAATTTGGGCCATAAAGAAAGTTCTTAGAAAGTGCAGAT 495
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTTATTTGAAGCAATTTAAACAT 180
Db 496 GACAAAATGGTTAAAAAAGATTGCAATGCGAGAAATCAAGTTACTAAGCAACTTAGGCAT 555
Qy 181 CCAAAATCTTGTGAACTCATCGAGTGTTCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 556 GAAAATCTTGTGAAATCTCTTGGAGGTGTGTAAGAAAAAAGAAAAACGATGTTACCTAGTCTTT 615
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAGAAAGAAACCCAAATGGAGTTGCTGAT 300

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Db 616 GAATTTGTTGACACACAAATCTTGATGACTTGGAGCTCTTCCAAATGGACTAGTAC 675
Qy 301 GGAGTATCAAAAGCGTATTATGCAACAACTTCAAGCTCTTAATTTCTGTATATACAT 360
Db 676 CAAGTAGTTCAAAAGTATTTGTTTTCAGATTTAATGGAATTTGATTTTGTACAGTCAC 735
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGNAATATC 420
Db 736 AATATACACAGAGATATAAAGCCAGAGAAATATATTAGTCTCCAGTCTGGCGTTGTC 795
Qy 421 AAGATTGTCAGCTTCGGGTTTGCAAAATCTG---ATTCCAGGAGATGCTTACACCGAT 477
Db 796 AAGCTATGCGATTTTGGATTTGCGGACATTTGCAGCTCTCGGGAGTTTATACATGAT 855
Qy 478 TATGTAGTACGAGATGCTACCGAGCTCTCGAACTTTCTTGGGAGATACCTAGTATGGT 537
Db 856 TATGTGCAACCCGATGGTACAGAGCTCCAGAACTATTGGTTGGTGTATGATCAAGTATGGC 915
Qy 538 TCTTCAGTGCATATATGGGCTATTGGTTGGTTTTCAGAGCTCTTCAGAGCCAGCCA 597
Db 916 AAGGCTCTTGATGTGGGCCATTTGGTTGTCTGGTAACTGAAATGTTTCATGGGGGAACCC 975
Qy 598 CTGTGGCCTGGAATCAGATGTGGCAACCTTTATCTGATAATCA 643
Db 976 CTATTCCTGAGATCTGATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1021

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RESULT 14

```

US-08-874-347-9
; Sequence 9, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,347
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055001
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...900

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OTHER INFORMATION:

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US-08-874-347-9
Query Match 15.7%; Score 163.8; DB 2; Length 903;
Best Local Similarity 55.3%; Pred. No. 1.6e-36;
Matches 365; Conservative 0; Mismatches 287; Indels 9; Gaps 2;
Qy 1 ATGGAAGAATGATGAAAATTTAGTAAAGCTGGAGAGGGCTTTATGGGGTTGTATTCAA 60
Db 1 ATGGAAGAATGATGAAAATTTAGTAAAGCTGGAGAGGGCTTTATGGGGTTGTATTCAA 60
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTTTAAATAAATTTGTTGGAATCTGAAGAT 120
Db 61 GCAAGAGATCTTGAAGTGGTACAAATTTAGTCTTTAAGAAATCCGATTTAGAGCAAA 120
Qy 121 GATCCTGTTCTTAAAGAAATAGCACTTAAGAGAAATAGTATGTTTGAAGCAATTTAAACAT 180
Db 121 GATGAGGAGTCTCTAGTACAGCAATTTCTGTAGATATCACTTTTGAAGAGATGCACAAT 180
Qy 181 CCAAACTTTGTGAACCTCATCGAGGTTTCAGAGAAAGAAAGAAATGCAATTTAGTTT 240
Db 181 GATAATGTTTGAAGCTTTTGAATATAAATTCATCAAGAGTCACTTTTATATCTTTGTTT 240
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATG-----GAGTT 294
Db 241 GAATTTCTTGTATCTTGAATTTTAAATAAAGTATATGAATAGTATTTCCAAAGGACATGATGCTT 300
Qy 295 GCTGATGGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCTAT 354
Db 301 GGTGCAAGATGATTAATAAAGTTTATGTCACAACTTGTATCAGGTGTTAATATTGTCTAT 360
Qy 355 ATACATAACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGA 414
Db 361 TCTCATCGTATTCTTCTCATCGTACTTGAAACCAACAAATCTTCTTATAGATCGAAGAGGA 420
Qy 415 ATAATCAGATTTGTGACTTCGGGTTTGCACAAA---TTCGTATCCAGAGATGCTCTAC 471
Db 421 AATCTTAAATTTAGCAGATTTTGGGCTTTCGAGGCGGTTTGGTGTCTTCCATTCGCGGTTAT 480
Qy 472 ACCGATTTATGTAGTACGAGATGTCACGAGCTCTGAACTCTTCTTGTGGAGATACCTCAG 531
Db 481 ACTCATGAGTTGTTTACACTTTGTTATCGTCTCCAGAGTTCTTTTAGTGGTTCGACAA 540
Qy 532 TATGGTTCTTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTCTGACAGGC 591
Db 541 TATGCAACAGCGCTTGATATATGAGCATTTGGATGATATTTTTCAGAAATGCGCTACAAA 600
Qy 592 CAGCCACTGGGCTGGAATATCAGATGTCGAGCACTTTATCTGATAATCAGACACTA 651
Db 601 AAGCCATTTATTCAGGTGATTTCTGAAATTTGTAATAATTTAGAAATATTAGAAATTA 660
Qy 652 G 652
Db 661 G 661

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RESULT 15

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US-09-093-522-9
; Sequence 9, Application US/09093522
; Patent No. 6015700
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN

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; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,522
; FILING DATE: 08-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874,347
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...900
; OTHER INFORMATION:
; US-09-093-522-9

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Query Match      15.7%; Score 163.8; DB 3; Length 903;
Best Local Similarity 55.2%; Pred.No.1.6e-36;
Matches 365; Conservative 0; Mismatches 287; Indels 9; Gaps 2;

QY 1 ATGGAAGATGATGAAAATTTAGCTTAAGACTGGAGAGGGCTTTATGGGTTGATTTCAAA 60
DB 1 ATGGAGCAATATCAGAGTTAGAGAGATTGGAGAGAGAACTTATGAGTTGTTTATAAA 60

QY 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
DB 61 GCAAAGGATCTTGAAGATGCTGACAAATTTAGCTCTTAAGAAAATCCGATTAGAAGCAGAA 120

QY 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAAT 180
DB 121 GATGAGGAGTTCTTAGTACAGCAATTCGTGAGATATCACTTTTGAAGAGAGATGCACAAT 180

QY 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240
DB 181 GATAATGTTGTAAGACTTTTGAATAAATTCATCAGAGTCAGCTTTATATCTTGTTTTT 240

QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAAGAAACCCAAATG-----GAGTT 294
DB 241 GAATTTCTTGATCTGATTTAAAAAAGTATATGATAGTATTCCTCAAGGACATGATGCTT 300

QY 295 GCTGATGGAGTGAATCAAAAGCGTATTATGCGCAACACTTCAAGCTTTAATTTCTGTCAT 354
DB 301 GGTGCAGAAATGNTTAAAGTTTATGTCACAACTTGATCAGGTGTTAAATATTGTCAT 360

QY 355 ATACATACTGTATTTCACAGAGATATAAAACCTGAAAATATTCTAATACTAAGCAAGGA 414
DB 361 TCTCATCGTATTCTTCATCGTGACTTGAACCCACAAAATCTTCTTATAGATCGAGAAGGA 420

QY 415 ATAATCAAGATTGTGACTTCGGGTTTGCACAAA---TTCTGATTCAGGAGATGCCTAC 471
DB 421 AATCTTAAATAGAGATTTCGGGCTTGCAGGGCGTTTGGGTTCCTCAATTCGCTGTTAT 480

QY 472 ACCGATTATGTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGAGATACCTCAG 531
DB 472 ACCGATTATGTAGTACGAGATGGTACCGAGCTCTTGTGGAGATACCTCAG 531

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Db 481 ACTCATGAAGTTGTTACACTTTGGTATCGTGCTCCAGAAGTTCTTTTAGGTGGTCGACAA 540
QY 532 TATGGTTCTTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTTCACAGGC 591
DB 541 TATGCAACAGCGCTTGATATATGGAGCATTTGGATGTTATTTTTCAGAAATGGCTACAAA 600
QY 592 CAGCACTGTGGCTGGAAAATCAGATGTGGACCAACTTTTATCTGATAATCAGAACACTA 651
DB 601 AAGCCATTATTTCCAGTGATTCTGAAATTTGATGAAATATTTAGAATATTTAGAATATTA 660
QY 652 G 652
DB 661 G 661

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Search completed: April 22, 2005, 01:29:29
Job time : 202.088 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:23:24 ; Search time 569.772 Seconds
(without alignments)
10815.645 Million cell updates/sec

Title: US-10-766-691-9
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870567 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1041	100.0	1041	4	AAD03816 Human kin
2	1025	98.5	1068	4	AAD03813 Human kin
3	839	80.6	945	4	AAD03817 Human kin
4	823	79.1	972	4	AAD03814 Human kin
5	821	78.9	1790	6	AAD30557 Human kin
6	762.8	73.3	1678	10	ABX08936 Human kin
7	757	72.7	1083	4	AAS06725 Polynucle
8	709	68.1	1819	4	AAD03818 Human kin
9	702	67.4	1266	12	ADK71927 Human kin
10	644	61.9	882	6	Aai64248 Human kin
11	604	58.0	1429	12	ADI40928 Human kin
12	543.2	52.2	1281	8	ABX34679 Human mdd
13	537	51.6	911	4	Aaf44669 Novel pro
14	537	51.6	911	12	ADI29367 Human MAR
15	454.4	43.7	561	4	AAD03812 Human kin
16	454.4	43.7	594	4	AAD03815 Human kin
17	453.2	43.5	2615	4	Aaf44670 Novel pro
18	453.2	43.5	2615	12	ADI29368 Mouse MAR
19	395	37.9	1086	10	ABZ77165 Human pro
20	343.8	33.0	1175	12	ADO01536 Human cyc

21	343.8	33.0	1178	12	ADO01535 Human cyc
22	343.8	33.0	1612	6	ABQ93433 Human CDN
23	343.8	33.0	2944	5	ABV24584 Human pro
24	251.8	24.2	1698	3	AAA29746 Rabbit KK
25	251.8	24.2	3080	3	AAA29745 Rabbit KK
26	242.2	23.3	1179	4	ABL12603 Drosophil
27	241.2	23.2	2095	10	ADC77658 Human 162
28	241.2	23.2	2095	13	ADQ89155 Human uro
29	202.6	19.5	1513	3	AAS21208 Human los
30	202.6	19.5	1513	12	ADI57213 Human NKI
31	202.6	19.5	1773	4	AAS06724 Polynucle
32	202.6	19.5	2503	13	ACN42574 Human dia
33	191	18.3	1667	3	AAS21207 Rat lost
34	191	18.3	1738	3	AAS21206 Rat lost
35	186.6	17.9	3297	4	ABL12602 Drosophil
36	177.4	17.0	1158	5	AAS70329 DNA encod
37	175.2	16.8	1866	4	AAP44672 Novel pro
38	175.2	16.8	1866	12	ADI29370 Human MAR
39	163.8	15.7	903	2	AAX07476 Pneumocys
40	162	15.6	1476	3	AAS237835 Cyclin-de
41	162	15.6	1635	2	AAV71074 Green flu
42	162	15.6	1635	2	AAV71073 CDK2-gree
43	161.6	15.5	1024	10	ABZ83372 Toxicolog
44	161.6	15.5	1297	6	ABQ60787 Human 10C
45	161.6	15.5	1297	10	ADD21391 Human cyc

ALIGNMENTS

RESULT 1
AAD03816
ID AAD03816 standard; cDNA; 1041 BP.
XX AC AAD03816;
XX DT 19-JUN-2001 (first entry)
XX DE Human kinase cDNA #5.
XX KW Human; kinase; gene therapy; bioreactor; mental disorder;
XX KW biological disorder; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1..1041
FT /*tag=a
FT /product= "Human kinase #5"
FT /note= "The coding region does not include stop codon"
XX PN WO200123579-A1.
XX PD 05-APR-2001.
XX PF 27-SEP-2000; 2000WO-US026621.
XX PR 28-SEP-1999; 99US-0156511P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX PI Sands AT;
XX DR WPI; 2001-266166/27.
XX DR P-PSDE; AAE00494.
XX PT New isolated human kinase polynucleotide useful for generating
XX PT antibodies, as reagents in diagnostic assays and for screening for
XX PT compounds useful for treating mental, biological or medical diseases.
XX PS Claim 1; Page 31-32; 38pp; English.

The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinases, the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 1041 BP; 344 A; 190 C; 228 G; 279 T; 0 U; 0 Other;

Query Match 100.0%; Score 1041; DB 4; Length 1041;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 1041; Conservative 0; Mismatches 0; Indels 0;

QY	1	ATGGAAGATGATAAAATTTAGCTAAGACTGGAGAAGGCTCTTATGCGGTGTGATTCAAA	60
Db	1	ATGGAAGATGATAAAATTTAGCTAAGACTGGAGAAGGCTCTTATGCGGTGTGATTCAAA	60
QY	61	TGCAGAAACAAACCTCTGGCAAGTACTAGCTGTATAAAATTTGTGGAACTGGAAGAT	120
Db	61	TGCAGAAACAAACCTCTGGCAAGTACTAGCTGTATAAAATTTGTGGAACTGGAAGAT	120
QY	121	GATCTGTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT	180
Db	121	GATCTGTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT	180
QY	181	CCAAATCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT	240
Db	181	CCAAATCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT	240
QY	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTCGTGAT	300
Db	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTCGTGAT	300
QY	301	GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTGCATATACAT	360
Db	301	GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTGCATATACAT	360
QY	361	AACTGTATTCCAGAGATATAAAACCTTGAAATATTTCTAATACTAAGCAAGGAATAATC	420
Db	361	AACTGTATTCCAGAGATATAAAACCTTGAAATATTTCTAATACTAAGCAAGGAATAATC	420
QY	421	AGATTCTGACTTCGGGTTTGCAAAATTTCTGATTCAGGAGATGCCTACACCGATTAT	480
Db	421	AGATTCTGACTTCGGGTTTGCAAAATTTCTGATTCAGGAGATGCCTACACCGATTAT	480
QY	481	GTAGCTACGAGATGGTACCGAGCTCCCTGAACTTCTGTGGGAGATACCTCAGATATGGTCT	540
Db	481	GTAGCTACGAGATGGTACCGAGCTCCCTGAACTTCTGTGGGAGATACCTCAGATATGGTCT	540
QY	541	TCAGTCGATATATGGGCTATTGGTTGGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG	600
Db	541	TCAGTCGATATATGGGCTATTGGTTGGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG	600
QY	601	TGGCTGGAAATCAGATGCGACCACTTTATCTGTAATCAGAACACTAGTAGAGACG	660
Db	601	TGGCTGGAAATCAGATGCGACCACTTTATCTGTAATCAGAACACTAGTAGAGACG	660
QY	661	GGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGCTCAAGTGATCCACTGCC	720

as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 1068 BP; 344 A; 197 C; 240 G; 287 T; 0 U; 0 Other;

Query Match 98.5%; Score 1025; DB 4; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 1.9e-263;
 Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAAAGTATGAAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
 1 ATGGAAAGTATGAAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTGTGGAACTCTGAAGAT 120
 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTGTGGAACTCTGAAGAT 120
 121 GATCCTGTGTTAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
 121 GATCCTGTGTTAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
 181 CCAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAAAGAAATGCATTAGTTTTT 240
 181 CCAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAAAGAAATGCATTAGTTTTT 240
 241 GAATACCTGTGATCATACCTTTTAAATGAGCTGGAGAGAAACCCAAATGGAGTTGCTGAT 300
 241 GAATACCTGTGATCATACCTTTTAAATGAGCTGGAGAGAAACCCAAATGGAGTTGCTGAT 300
 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCAATACAT 360
 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCAATACAT 360
 361 AACTGTATTTCACAGAGATATAAAACCTGAAAAATATTCTAATACTAAGCAAGGAATAATC 420
 361 AACTGTATTTCACAGAGATATAAAACCTGAAAAATATTCTAATACTAAGCAAGGAATAATC 420
 421 AAGATTGTGATCTCGGGTTTGCAAAATTCGATTCAGAGAGATGCCATACCGGATTAT 480
 421 AAGATTGTGATCTCGGGTTTGCAAAATTCGATTCAGAGAGATGCCATACCGGATTAT 480
 481 GTAGCTAGGATGGTACCGAGCTCCTGAACCTCTTGTGGGAGATACCTCAGTATGGTTCT 540
 481 GTAGCTAGGATGGTACCGAGCTCCTGAACCTCTTGTGGGAGATACCTCAGTATGGTTCT 540
 541 TCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCCTGACAGGCCAGCCACTG 600
 541 TCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCCTGACAGGCCAGCCACTG 600
 601 TGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACATAGTAGAGAG 660
 601 TGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACATAGTAGAGAG 660
 661 GGGTTTCGCCATGTTGACCGCTGGTCTCGAACTCTTGAGCTCAAGTATCCACCTGCC 720
 661 GGGTTTCGCCATGTTGACCGCTGGTCTCGAACTCTTGAGCTCAAGTATCCACCTGCC 720

721 GTAGCCTCTCAAGTGTGGAAATTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
 721 GTAGCCTCTCAAGTGTGGAAATTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
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 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGGTGCTGAAG 900
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RESULT 3
 AAD03817
 ID AAD03817 standard; cDNA; 945 BP.
 XX AAD03817;
 XX 19-JUN-2001 (first entry)
 XX Human kinase cDNA #6.
 XX Human; kinase; gene therapy; bioreactor; mental disorder;
 XX biological disorder; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 CDS 1..945
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 FT /product= "Human kinase #6"
 FT /note= "The coding region does not include stop codon"
 FT /partial
 XX MO200123579-A1.
 XX 05-APR-2001.
 XX 27-SEP-2000; 2000MO-US026621.
 XX 28-SEP-1999; 99US-0156511P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX WPI; 2001-266166/27.
 DR P-PSDB; AAE00495.
 XX
 PT New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX
 PS Claim 3; Page 33; 38pp; English.
 XX
 CC The present sequence is a cDNA encoding novel human protein (NHP) known
 CC as human kinase. The human kinases share structural similarity with
 CC animal kinases, more particularly serine or threonine protein kinases.

Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 945 BP; 323 A; 165 C; 202 G; 255 T; 0 U; 0 Other;
 Query Match 80.6%; Score 839; DB 4; Length 945;
 Best Local Similarity 90.8%; Pred. No. 9e-214;
 Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 1 ATGGAAGATGATAAAATTAAGCTAAGCTGAGAGGGCTTAATGGGTTGTAATCAAA 60
 1 ATGGAAGATGATAAAATTAAGCTAAGCTGAGAGGGCTTAATGGGTTGTAATCAAA 60
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 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTGTTAAAAATTTGGGAATCTGAAGAT 120
 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACACAT 180
 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACACAT 180
 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAAAGGAAATGCAATTTAGTTTTT 240
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 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAACCCCAATGAGTTGCTGAT 300
 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAACCCCAATGAGTTGCTGAT 300
 301 GGAGTGATCAAAAGCGTATTATGCAAACTTCAAGCTCTTAATTTCTGTATATACAT 360
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 361 AACTGTATTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC 420
 361 AACTGTATTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC 420
 421 AAGATTGTGACATTCGGGTTTGACAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
 421 AAGATTGTGACATTCGGGTTTGACAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
 481 GTAGCTACAGAGATGATACCGAGTCTCTGAATCTTTGTGGAGATACCTAGTATGTTCT 540
 481 GTAGCTACAGAGATGATACCGAGTCTCTGAATCTTTGTGGAGATACCTAGTATGTTCT 540
 541 TCAGTGCATATATGGGCTATTTGTTGTTTTCAGAGCTCTCTGAGGAGATCTCAGTATGTTCT 600
 541 TCAGTGCATATATGGGCTATTTGTTGTTTTCAGAGCTCTCTGAGGAGATCTCAGTATGTTCT 600
 601 TGCCCTGGAAATCAGATGTGGACCACTTTATCTGATATCAGAACACTAGTAGAGACG 660
 601 TGCCCTGGAAATCAGATGTGGACCACTTTATCTGATATCAGAACACTAGTAGAGACG 660
 661 GGGTTTGGCAATTTGACCAAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCACCTGCC 720
 651 -----
 721 GTAGCCTCTCAAAGTGTGGAATTTACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780

651 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 684
 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACTCTT 840
 685 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACTCTT 744
 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGTCTGAACTTCAATGAAGGGGTGTCTGAAG 900
 745 GAGGAAAGTTCTCAGATGTTTCATCTGTGGTCTGAACTTCAATGAAGGGGTGTCTGAAG 804
 901 ATGAATCCAGATCAGATTAACCTGTTCCCAACTCTCTGAGAGCTCTACTTTGATTCT 960
 805 ATGAATCCAGATCAGATTAACCTGTTCCCAACTCTCTGAGAGCTCTACTTTGATTCT 864
 961 TTTCAAGAGGCCCAAAATTAAGAGAAAGACGTAATGAAGGAAAGAACAGAGACGCCAA 1020
 865 TTTCAAGAGGCCCAAAATTAAGAGAAAGACGTAATGAAGGAAAGAACAGAGACGCCAA 924
 1021 CAGGTACTTCCGCTCAAAAGT 1041
 925 CAGGTACTTCCGCTCAAAAGT 945
 RESULT 4
 AAD03814
 ID AAD03814 standard; cDNA; 972 BP.
 XX AAD03814;
 AC AAD03814;
 XX 19-JUN-2001 (first entry)
 DT 19-JUN-2001 (first entry)
 XX Human kinase cDNA #3.
 DE Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder; ss.
 XX Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 1..972
 FT /tag= a
 FT /product= "Human kinase #3"
 FT /note= "The coding region does not include stop codon"
 XX
 PN WO200123579-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-US026621.
 XX
 PR 28-SEP-1999; 99US-0156511P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX
 DR WPI; 2001-266166/27.
 DR P-PSDB; AAE00492.
 XX
 PT New isolated human kinase polynucleotide useful for generating for
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX
 PS Disclosure; Page 29-30; 38pp; English.
 XX
 CC The present sequence is a cDNA encoding novel human protein (NHP) known
 CC as human kinase. The human kinases share structural similarity with
 CC animal kinases, more particularly serine or threonine protein kinases.
 CC Human kinase cDNA is useful for the detection of mutant human kinase for
 CC the diagnosis of disease, and also as a therapeutic. It is useful for

screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 972 BP: 323 A; 172 C; 214G; 263 T; 0 U; 0 Other;

```
Query Match          79.1%; Score 823; DB 4; Length 972;
Best Local Similarity 90.6%; Pred. No. 1.7e-209;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1
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Qy	1	ATGGAAGATGTAATAATTAAGCTGGAGAGGGTCTTATGGGGTGTATTCAAA	60
Db	1	ATGGAAGATGTAATAATTAAGCTGGAGAGGGTCTTATGGGGTGTATTCAAA	60
Qy	61	TGCAGAAACAAAACCTCTGGACAAGTAGCTGTTTAAAAAATTTGTGGAATCTCAAGAT	120
Db	61	TGCAGAAACAAAACCTCTGGACAAGTAGCTGTTTAAAAAATTTGTGGAATCTCAAGAT	120
Qy	121	GATCCTGTGTTTAAAGAAAATAGCACTAAGAGAAAATACGTATGTTGAAGCAATTAAGAAAT	180
Db	121	GATCCTGTGTTTAAAGAAAATAGCACTAAGAGAAAATACGTATGTTGAAGCAATTAAGAAAT	180
Qy	181	CCAAATCTGTGGAACCTCATCGAGGTGTTTCAAGAGAAAAGGAAAATGCAATTAAGTTTTT	240
Db	181	CCAAATCTGTGGAACCTCATCGAGGTGTTTCAAGAGAAAAGGAAAATGCAATTAAGTTTTT	240
Qy	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATTTGGAGTTGCTGAT	300
Db	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATTTGGAGTTGCTGAT	300
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Db	301	GGAGTGATCAAAAGCGTATTATGGCAACACATTCGAAGCTCTTAATTTCTGTGCATATACAT	360
Qy	361	AACGTGATTACAGAGATATAAAACCTGAGAAATATTCTTAATACTAAGCAAGGAATAATC	420
Db	361	AACGTGATTACAGAGATATAAAACCTGAGAAATATTCTTAATACTAAGCAAGGAATAATC	420
Qy	421	AAGATTGTGACTTTCGGGTTTGCAAAATCTTGATTCAGAGAGATGCCTACACCGATTAT	480
Db	421	AAGATTGTGACTTTCGGGTTTGCAAAATCTTGATTCAGAGAGATGCCTACACCGATTAT	480
Qy	481	GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTTGGGAGATACCTCAGTATGGTTCT	540
Db	481	GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTTGGGAGATACCTCAGTATGGTTCT	540
Qy	541	TCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCACTG	600
Db	541	TCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCACTG	600
Qy	601	TGGCCTGGAAATCAGATGTGGACCACTTTATCTGTAATAACAGAACTAGTAGAGACG	660
Db	601	TGGCCTGGAAATCAGATGTGGACCACTTTATCTGTAATAACAGAACTAGTAGAGACG	660
Qy	661	GGGTTTCGCCATGTGACACGGCTGGTTCGAACTCTTGAAGTCAAGTGCACCTGCC	720
Db	651	-----	650
Qy	721	GTAGCCTCTCAAAGTGCTGGAAATTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTT	780
Db	651	-----AGGAAAAATTAATCCCAAGACATCAATCAATCTTT-----	684

Qy	781	AAAAGTAAACGGGTTTTTCCTATGGCATCAGTATACTTGAGCCAGAAGACATGGAACA	CTTT	840
Db	685	AAAAGTAACCGGTTTTTCCTATGGCATCAGTATACTTGAGCCAGAAGACATGGAACA	CTTT	744
Qy	841	GAGGAAAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCATGAAGGGGTGTC	TGAAG	900
Db	745	GAGGAAAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCATGAAGGGGTGTC	TGAAG	804
Qy	901	ATGAAATCCAGATGACAGATTAACTGTGCCAATCTCTGGAGAGCTCCTAC	CTTTGATTC	960
Db	805	ATGAATCCAGATGACAGATTAACTGTGCCAATCTCTGGAGAGCTCCTAC	CTTTGATTC	864
Qy	961	TTTTCAGAGGCCCAAAATTTAAAGAAAAAGCACGTAAATGAAGGAAGAAAACAGAA	GACGCCAA	1021
Db	865	TTTTCAGAGGCCCAAAATTTAAAGAAAAAGCACGTAAATGAAGGAAGAAAACAGAA	GACGCCAA	924
Qy	1021	CAGGT	1025	
Db	925	CAGGT	929	

RESULT 5

AAD30557	
ID	AAD30557 standard; cDNA; 1790 BP.
XX	
XX	
AC	AAD30557;
XX	
DT	21-MAY-2002 (first entry)
XX	
DE	Human kinase polypeptide (PKIN-10) cDNA.
XX	
KW	Human; kinase polypeptide; PKIN-10; gene
KW	leukaemia; immune disorder; lymphoma; melanoma
KW	acquired immunodeficiency syndrome; AIDS; aschima; Crohn's disease; rheumatoid arthritis; cirrhosis; hepatitis; psoriasis; Cushing's cholestasis; cardiac; cardiovascular diseases; lipid disorder; fatty liver; Gaucher's disease screening; transgenic animal; anti-drug hypersensitive; anti-HIV; enzyme; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 239..1267
FT	/tag= a
FT	/product= "Human PKIN-10"

WO200208399-A2

31-JAN-2002

20-JUL-2001: 2001WO-US023092

21-JUL-2000: 2000US-0220038P.

28-JUL-2000; 2000US-0222112P
04-AUG-2000; 2000US-0222831P

11-AUG-2000; 2000US-0224/29P.

(INCY-) INCYTE GENOMICS INC.
(THOR/) THORNTON M.

Thornton M. Yue H. Khan FA.

Patterson C, Ramkumar J, Triboulev CM, Bandman O.

Yao MG, Elliott VS, Recipon Tang YT, Xu Y. Walsh RT. G

WPT: 2002-206083/26.

P-PSDB; AAE19152.

New human kinase polypeptide,

PT treatment of cancer, immune disorder, growth and developmental disorder,
 XX cardiovascular disorder and lipid disorder.
 PS Claim 5; Page 183; 196pp; English.
 XX

CC The present invention relates to an isolated human kinase polypeptide
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
 CC useful for diagnosing, treating and preventing cancer (e.g., leukemia,
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
 CC buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
 CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis.
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 CC drug screening techniques and to analyse the proteome of a tissue or cell
 CC type. PKIN is useful for creating knockin humanised animals or transgenic
 CC animals to model human diseases, in somatic or germline gene therapy, to
 CC generate a transcript image of a tissue or cell type, for detecting
 CC differences in the chromosomal location due to translocation, inversion,
 CC etc., among normal, carrier or affected individuals, and as hybridisation
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful
 CC in southern or northern analysis, dot blot or other membrane-based
 CC technologies, in PCR technologies, in dipstick, pin, multiformat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-10 cDNA

XX SQ Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 U; 0 Other;

Query Match 78.9%; Score 821; DB 6; Length 1790;
 Best Local Similarity 90.6%; Pred. No. 7.4e-209;
 Matches 927; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 1 ATGGAAGATGATGAAATAGCTAGCACTGGAGAGGGCTTATGGGTGATTTCAAA 60
 DB 239 ATGGAAGATGAAATAGCTAGCACTGGAGAGGGCTTATGGGTGATTTCAAA 298
 QY 61 TGCAGAACAAACCTCTGGCAAGTAGTAGCTTTAAAAAATTTGGGAATCTGAAGAT 120
 DB 299 TGCAGAACAAACCTCTGGCAAGTAGTAGCTTTAAAAAATTTGGGAATCTGAAGAT 358
 QY 121 GATCCTCTTTAAGAAATAGCACTAGAGAAATAGCTATGTTGAAGCAATTAACAAT 180
 DB 359 GATCCTCTTTAAGAAATAGCACTAGAGAAATAGCTATGTTGAAGCAATTAACAAT 418
 QY 181 CCAATCTTGTGAACCTCATCGAGTCTTCAGAGAAAGAAAGAAATGCAATTTAGTTTT 240
 DB 419 CCAATCTTGTGAACCTCATCGAGTCTTCAGAGAAAGAAAGAAATGCAATTTAGTTTT 478
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCAATGAGTGTCTGAT 300
 DB 479 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCAATGAGTGTCTGAT 538
 QY 301 GGAGTGTATCAAGCGTATTATGCAACACTTCAAGCTCTTAAATCTGTCATATACAT 360
 DB 539 GGAGTGTATCAAGCGTATTATGCAACACTTCAAGCTCTTAAATCTGTCATATACAT 598
 QY 361 AACTGTATTACAGAGATATAAAACCTTGAATAATTTCTAATACTAAGCAAGCAATAATC 420
 DB 599 AACTGTATTACAGAGATATAAAACCTTGAATAATTTCTAATACTAAGCAAGCAATAATC 658
 QY 421 AGAATTTGTGACTTCGGGTTTGCAAAATTTCTGATTTCCAGGAGATGCTACACCGATTAT 480
 DB 659 AGAATTTGTGACTTCGGGTTTGCAAAATTTCTGATTTCCAGGAGATGCTACACCGATTAT 718
 QY 481 GTAGCTACGAGATGGTACCGAGTCTCTGAACCTTCTGTGGGATACCTAGTATGTTCT 540
 DB 719 GTAGCTACGAGATGGTACCGAGTCTCTGAACCTTCTGTGGGATACCTAGTATGTTCT 778
 QY 541 TCAGTCGATATATGGGCTATTTGTTGTTTTTGCAGAGCTCTCTGACAGCCAGCCACTG 600
 DB 779 TCAGTCGATATATGGGCTATTTGTTGTTTTTGCAGAGCTCTCTGACAGCCAGCCACTG 838

QY 601 TGGCCTCGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGTAGAGACG 660
 DB 839 TGGCCTCGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACT----- 888
 QY 661 GGGTTTCGCCATGTTGACCAAGGCTGGTCTCGAACTCTTTGACGTCAAGTGATCCACCTGCC 720
 DB 889 ----- 888
 QY 721 GTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAATTAATCCCAAGACATCAATCAATCTTT 780
 DB 889 -----AGGAAAATTAATCCCAAGACATCAATCAATCTTT 922
 QY 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGACATGGAACCTTT 840
 DB 923 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGACATGGAACCTTT 982
 QY 841 GAGGAAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTTCATGAAGGGTGTCTGAAG 900
 DB 983 GAGGAAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTTCATGAAGGGTGTCTGAAG 1042
 QY 901 ATGAATCCAGATGACAGATTAACTGTTTCCAACTCTCTGGAGAGCTCTACTTTGATCT 960
 DB 1043 ATGAATCCAGATGACAGATTAACTGTTTCCAACTCTCTGGAGAGCTCTACTTTGATCT 1102
 QY 961 TTTCAAGAGGCCCAAAATTAAGAAAAGGACGTAATGAAGGAAAGAAACAGAACGCCAA 1020
 DB 1103 TTTCAAGAGGCCCAAAATTAAGAAAAGGACGTAATGAAGGAAAGAAACAGAACGCCAA 1162
 QY 1021 CAG 1023
 DB 1163 CAG 1165
 RESULT 6
 ABX08936
 ID ABX08936 standard; cDNA; 1678 BP.
 XX AC ABX08936;
 XX AC
 DT 21-JAN-2003 (first entry)
 XX
 DE cDNA encoding human DITHP protein #6.
 XX
 KW Human; ss; gene; diagnostic and therapeutic; DITHP; cancer;
 KW arteriosclerosis atherosclerosis; psoriasis; asthma; autoimmune thyroiditis;
 KW autoimmune; inflammatory; anaemia; diabetes mellitus; glomerulonephritis; gout; stroke;
 KW Crohn's disease; rheumatoid arthritis; uveitis; AIDS; allergy;
 KW multiple sclerosis; immunodeficiency disease; neurological disorder; epilepsy;
 KW Alzheimer's disease; dementia; mental retardation; gastrointestinal;
 KW Parkinson's disease; ulcer; cirrhosis; reproductive; infertility;
 KW endometriosis; endocrine disorder; hyperparathyroidism; hyperlipidemia;
 KW hypercholesterolaemia; hypoglycaemia; obesity; Reiter's syndrome;
 KW connective tissue disorder; osteoporosis; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200279473-A2.
 XX
 PD 10-OCT-2002.
 XX
 XX 09-JAN-2002; 2002WO-US001009.
 XX
 XX 12-JAN-2001; 2001US-0261622P.
 PR 16-JAN-2001; 2001US-0261864P.
 PR 16-JAN-2001; 2001US-0261865P.
 PR 17-JAN-2001; 2001US-0262164P.
 PR 17-JAN-2001; 2001US-0262207P.
 PR 17-JAN-2001; 2001US-0262208P.
 PR 17-JAN-2001; 2001US-0262209P.
 PR 17-JAN-2001; 2001US-0262215P.
 PR 18-JAN-2001; 2001US-0263102P.

PR	19-JAN-2001; 2001US-0262599P.	
PR	19-JAN-2001; 2001US-0262662P.	
PR	19-JAN-2001; 2001US-0262760P.	
PR	19-JAN-2001; 2001US-0263063P.	
PR	19-JAN-2001; 2001US-0263064P.	
PR	19-JAN-2001; 2001US-0263065P.	
PR	19-JAN-2001; 2001US-0263069P.	
PR	19-JAN-2001; 2001US-0263077P.	
PR	19-JAN-2001; 2001US-0263329P.	
PR	19-JAN-2001; 2001US-0263330P.	
XX	(INCY-) INCYTE GENOMICS INC.	
XX	Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;	
PI	Dam TC, Liu TP, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;	
PI	Chang SC, Gerstein EH, Peralta CH, David MH, Lewis SA;	
XX	WPI; 2003-040680/03.	
DR	P-PSDB; ABU05290.	
XX	New human diagnostic and therapeutic (DITHP) polynucleotides and	
PT	polypeptides, useful for diagnosing, preventing or treating diseases,	
PT	e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory	
PT	diseases.	
XX		
XX	Claim 1; Page 267; 331pp; English.	
XX	This invention relates to the cDNA and protein sequences of fifty six	
CC	polynucleotides for diagnostics and therapeutics (DITHP). The human DITHP	
CC	polynucleotides and polypeptides are useful for diagnosing, preventing or	
CC	treating diseases associated with, as well as effects of exogenous	
CC	compounds, on the expression of human molecules, such as cell	
CC	proliferative diseases (e.g. cancer, arteriosclerosis atherosclerosis,	
CC	psoriasis, primary thrombocytopenia), autoimmune/inflammatory diseases	
CC	(e.g. anaemia, asthma, autoimmune thyroiditis, Crohn's disease, diabetes	
CC	mellitus, glomerulonephritis, gout, multiple sclerosis, rheumatoid	
CC	arthritis, uveitis, acquired immunodeficiency disease; AIDS; allergies;	
CC	neurological disorders (e.g. stroke, Alzheimer's disease, dementia,	
CC	mental retardation, Parkinson's disease, epilepsy), gastrointestinal	
CC	(e.g. ulcer, cirrhosis), reproductive (e.g. infertility, endometriosis),	
CC	endocrine disorders (e.g. hyperparathyroidism, hypercholesterolaemia,	
CC	hypoglycaemia, hyperlipidemia, obesity), connective tissue disorders	
CC	(e.g. osteoporosis, Reiter's syndrome), or infections (e.g. bacterial,	
CC	viral, fungal, parasitic, protozoal). The DITHP sequences may be used to	
CC	generate hybridisation probes useful in chromosomal mapping of naturally	
CC	occurring genomic sequences. They are also useful in designing probes	
CC	useful in diagnostic assays. The polynucleotides are useful as molecular	
CC	weight markers, or as antigen to elicit an immune response. The present	
CC	sequence represents a human diagnostics and therapeutics (DITHP) cDNA	
XX	sequence of the invention	
XX		
SQ	Sequence 1678 BP; 541 A; 308 C; 336 G; 493 T; 0 U; 0 Other;	
	Query Match 73.3%; Score 762.8; DB 10; Length 1678;	
	Best Local Similarity 90.0%; Pred. No. 2.6e-193;	
	Matches 925; Conservative 0; Mismatches 2; Indels 101; Gaps 6;	
QY	1 ATCGAAAGATGAAAAATTAGCTTAAGCTTGGAGAGGGTCTTATGGGTTGTATTCAA 60	
DB	131 ATCGAGAGATGAAAAATTAGCTTAAAGCTGGAGAGGGTCTTATGGGTTGTATTCAA 190	
QY	61 TGCAGA-AACAAACCTCTGGCAAGTAGTAGCTTTAAAAATTTTGTGGAATCTGAAGA 119	
DB	191 TGCAGATACAAACCTCTGGCAAGTAGTAGCTTTAAAAATTTTGTGGAATCTGAAGA 250	
QY	120 TGATCCTGTTGTTTAAGAAAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAGAA 178	
DB	251 TGATCCTGTTGTTTAAGAAAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAGAA 310	
QY	179 ATCCAAATCTTGAAACCTCATCGAGGTGTTTCAGAGAAAAAGAAAAATGCAATTAGTTT 238	
DB	311 ATCCAAATCTTGAAACCTCATCGAGGTGTTTCAGAGAAAAAGAAAAATGCAATTAGTTT 370	

XX W0200123579-Al.
 XX 05-APR-2001.
 XX 27-SEP-2000; 2000WO-US026621.
 XX 28-SEP-1999; 99US-0156511P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 XX Sands AT;
 XX WPI; 2001-266166/27.
 XX P-PSDB; AAE00490.
 XX New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX PS Disclosure; Page 34-35; 38pp; English.
 XX The present sequence encodes a novel human protein (NHP) which is a human
 CC kinase. A polymorphism was identified in the 3' UTR of the present
 CC sequence. The human kinases share structural similarity with animal
 CC kinases, more particularly serine or threonine protein kinases. Human
 CC kinase cDNA is useful for the detection of mutant human kinase for the
 CC diagnosis of disease, and also as a therapeutic. It is useful for
 CC screening drugs effective in the treatment of symptomatic or phenotypic
 CC manifestations perturbing the normal function of NHP in the body. The NHP
 CC nucleotide sequences are useful for generation of antibodies, as reagents
 CC in diagnostic assays, for the identification of other cellular gene
 CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX SQ Sequence 1819 BP; 539 A; 368 C; 406 G; 505 T; 0 U; 1 Other;
 Query Match 68.1%; Score 709; DB 4; Length 1819;
 Best Local Similarity 77.0%; Pred. No. 6.2e-179;
 Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;
 QY 1 ATGGAAGATGATGAAAAATTAGCTAAGACTGGAGAGGGCTTATGGGGTTGTATTCAAA 60
 DB 138 ATGGAAGATGATGAAAAATTAGCTAAGACTGGAGAGGGCTTATGGGGTTGTATTCAAA 197
 QY 61 TGCAGAAACAAACCTCTGGACAAAGTAGTAGCTGTAAAAAAATTTGGAAATCTGAAGAT 120
 DB 198 TGCAGAAACAAACCTCTGGACAAAGTAGTAGCTGTAAAAAAATTTGGAAATCTGAAGAT 257
 QY 121 GATCCTCTGTTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 180
 DB 258 GATCCTCTGTTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 317
 QY 181 CCAAACTCTGTGAACCTCATCGAGGTGTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
 DB 318 CCAAACTCTGTGAACCTCATCGAGGTGTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 377
 QY 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
 DB 378 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 437
 QY 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360

DB 438 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 497
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATAATTTCTAAATACTAAGCAAGGAATATC 420
 DB 498 AACTGTATTACAGAGATATAAAACCTGAAATAATTTCTAAATACTAAGCAAGGAATATC 557
 QY 421 AAGATTTGTGACTTCGGGTTTGGACAATTTCTG----- 453
 DB 558 AAGATTTGTGACTTCGGGTTTGGACAATTTCTGAGTTGGACTTCATCTTTCTCTGGTGCC 617
 QY 454 ----- 453
 DB 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAAATTTCTTTCTGCCAATTCAGAGATTTTT 677
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 DB 678 CTCCTGGCTTGGATCCATTGCTGACACAGTGTTCACCATGGGGCCCGGCTCATCTCGA 737
 QY 454 ----- 453
 DB 738 ACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCCTCCAAAGTCTGGATTGCAAGTGTG 797
 QY 454 ----- 453
 DB 798 AGCCACCGTCCCGCAGCCAGATTTTCAACAATACTACTGAGAGCTCACAAGATTGTTT 857
 QY 454 -----ATTCCAGGAGATGCCCTACACC 474
 DB 858 TTAGTGGGAACACAAATTTTCGAACAAATTTCTTGAGAACGCATTCAGGAGATGCCCTACACC 917
 QY 475 GATTATGTAGCTAGCAGATGGTACCGAGCTCTCGAACTTCTTTGGGGAGATACCTCAGTAT 534
 DB 918 GATTATGTAGCTAGCAGATGGTACCGAGCTCTCGAACTTCTTTGGGGAGATACCTCAGTAT 977
 QY 535 GGTTCCTCAGTCAGATATATGGGCTATTGTTGTTTTCGAGAGCTCTTGACAGGCGCAG 594
 DB 978 GGTTCCTCAGTCAGATATATGGGCTATTGTTGTTTTCGAGAGCTCTTGACAGGCGCAG 1037
 QY 595 CCACTGTGGCTCGAAATCAGATGTGGACCAACTTTTATCTGATAATCAGAACTAGTA 654
 DB 1038 CCACTGTGGCTCGAAATCAGATGTGGACCAACTTTTATCTGATAATCAGAACTAGTA 1097
 QY 655 GAGACGGGGTTTCGCATGTTGACCGGCTGTTCTGAACTCTTGAGCTCAAGTGATCCA 714
 DB 1098 GAGACGGGGTTTCGCATGTTGACCGGCTGTTCTGAACTCTTGAGCTCAAGTGATCCA 1157
 QY 715 CCTGCGCTAGCCTCTCAAGTGTCTGGAATTTACAGGAAAAATTAATCCCAAGACATCAATCA 774
 DB 1158 CCTGCGCTAGCCTCTCAAGTGTCTGGAATTTACAGGAAAAATTAATCCCAAGACATCAATCA 1217
 QY 775 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGA 834
 DB 1218 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGA 1277
 QY 835 ACTCTTGAGAAAGTTCTCAGATGTTTCATCTCTGTGGCTCTGAACTTCTGAAGGGGTGT 894
 DB 1278 ACTCTTGAGAAAGTTCTCAGATGTTTCATCTCTGTGGCTCTGAACTTCTGAAGGGGTGT 1337
 QY 895 CTGAAGATGAATCCAGATGACAGTTAACTGTTCCCACTCTCTGGAGAGCTCTCTACTTTT 954
 DB 1338 CTGAAGATGAATCCAGATGACAGTTAACTGTTCCCACTCTCTGGAGAGCTCTCTACTTTT 1397
 QY 955 GATTCTTTTCAAGAGGGCCCAAAATTAAGAAAAAGCAGCTAATGAAGGAAGAAACAGAGA 1014
 DB 1398 GATTCTTTTCAAGAGGGCCCAAAATTAAGAAAAAGCAGCTAATGAAGGAAGAAACAGAGA 1457
 QY 1015 CGCCCAACAGGT 1025
 DB 1458 CGCCCAACAGGT 1468
 RESULT 9
 ADK71927

ADK71927 standard; cDNA; 1266 BP.
ADK71927;
20-MAY-2004 (first entry)
Human kinase and phosphatase KPP-45 cDNA.
human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
hypotensive; vasotropic; antiinflammatory; antiangiinal; anti-HIV;
antiallergic; antiasthmatic; immunosuppressive; antichyroid;
dermatologic; antidiabetic; nephrotropic; antitumor; gastrointestinal;
neuroprotective; osteopathic; antirheumatic; uropathic; ophthalmological;
antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
antiparasitic; haemostatic; cytostatic; antilipemic; antiparasitic;
antihelminthic; antibacterial; virucide; protozoacide; fungicide;
cardiovascular disease; immune system; neurological; growth; development;
cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
helminthic infection; transgenic; gene therapy; ss; gene.
Homo sapiens.
W02004018641-A2.
04-MAR-2004.
25-AUG-2003; 2003WO-US026635.
26-AUG-2002; 2002US-0406172P.
25-SEP-2002; 2002US-0413910P.
27-SEP-2002; 2002US-0414296P.
11-OCT-2002; 2002US-0417821P.
(INCY-) INCYTE CORP.
Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
Murage J;
WPI; 2004-226830/21.
P-PSDB; ADK71869.
New human kinases and phosphatases, useful for diagnosing, treating or
preventing atherosclerosis, hypertension, AIDS, allergy, multiple
sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
or hepatitis.
Claim 5; SEQ ID NO 104; 347pp; English.
The invention relates to a novel isolated polypeptide which is a human
kinase and phosphatase (KPP). The polypeptide of the invention
demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic,
antisthmatic, immunosuppressive, antichyroid, dermatological,
antidiabetic, nephrotropic, antitumor, gastrointestinal, neuroprotective,
osteopathic, antirheumatic, uropathic, ophthalmological, antiparasitic,
antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antiparasitic,
haemostatic, cytostatic, antilipemic, antiparasitic, antihelminthic,
antibacterial, virucide, protozoacide and fungicide activities. The
kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
antagonists may be useful for diagnosing, treating or preventing
disorders such as cardiovascular diseases, immune system disorders,
neurological disorders, disorders affecting growth and development, cell
proliferative disorders and viral, bacterial, fungal, parasitic, cell
protozoan or helminthic infections. Furthermore, the molecules of the
invention may be useful for creating transgenic animals to model human
disease and during gene therapy. The current sequence is that of a human
KPP cDNA of the invention.
Sequence 1266 BP; 414 A; 234 C; 254 G; 364 T; 0 U; 0 Other;

Query Match 67.4%; Score 702; DB 12; Length 1266;
Best Local Similarity 81.9%; Pred. No. 4e-177;
Matches 927; Conservative 0; Mismatches 0; Indels 205; Gaps 2;
QY 1 ATGAAAAGTATGAAAAATTTAGCTAGCTGGAGAGGGTCTTATGGGGTGTGATTTCAAA 60
DB 54 ATGAAAAGTATGAAAAATTTAGCTAGCTGGAGAGGGTCTTATGGGGTGTGATTTCAAA 113
QY 61 TGCAGAAACAAAACCTCTGCAAGTAGTAGCTGTGTTAAAAAATTTGTTGGAATCTGAAGAT 120
DB 114 TGCAGAAACAAAACCTCTGCAAGTAGTAGCTGTGTTAAAAAATTTGTTGGAATCTGAAGAT 173
QY 121 GATCCTGTTCTTAAAGAAAATAGCACTAAGAGAAATAGTATGTTGAGCAATTAACACAT 180
DB 174 GATCCTGTTCTTAAAGAAAATAGCACTAAGAGAAATAGTATGTTGAGCAATTAACACAT 233
QY 181 CCAAAATCTTGTGAACCTCATCTGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
DB 234 CCAAAATCTTGTGAACCTCATCTGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 293
QY 241 GAATACCTGTGATCATATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 300
DB 294 GAATACCTGTGATCATATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 353
QY 301 GGAGTGATCAAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGCTCATATACAT 360
DB 354 GGAGTGATCAAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGCTCATATACAT 413
QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTAATAAATAAGCAAGAAATAATC 420
DB 414 AACTGTATTACAGAGATATAAAACCTGAAATATTCTAATAAATAAGCAAGAAATAATC 473
QY 421 AGATTTGTGACTTCGGGTTCGCAAAATTTCTGA----- 454
DB 474 AGATTTGTGACTTCGGGTTCGCAAAATTTCTGA----- 533
QY 455 ----- 454
DB 534 TCCTTGATTGGCTTAATAGTTGACCTTCTGAATTTCTTTCTGCCAATTCAGAGATTTTC 593
QY 455 -----TTCAGAGAGATGCTACACCGATTATGTAGTACGAG 491
DB 594 TCCTTGATTGGCTTAATAGTTGACCTTCTGAATTTCTTTCTGCCAATTCAGAGATTTTC 653
QY 492 ATGTTACCCAGCTCCTGAACTTCTGTTGGAGATCTCAGTATGTTCTTCAGTCCGATAT 551
DB 654 ATGTTACCCAGCTCCTGAACTTCTGTTGGAGATCTCAGTATGTTCTTCAGTCCGATAT 713
QY 552 ATGGGCTATTGGTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCACTGTGGCCTCGAAA 611
DB 714 ATGGGCTATTGGTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCACTGTGGCCTCGAAA 773
QY 612 ATCAGATGTGGACCAACTTTATCTGATATACAGACACTAGTAGAGACGGGGTTTCGCCA 671
DB 774 ATCAGATGTGGACCAACTTTATCTGATATACAGACACT----- 812
QY 672 TGTGTACACAGGCTGGTCTCGAACTCTTTGACGTCAAGTGATCCACCTGCGTAGCTCTCA 731
DB 813 ----- 812
QY 732 AAGTGTGGAATTAACAGGAAATTAATCCAAAGACATCAATCAATCTTTTAAAGTAACGG 791
DB 813 -----AGGAAATTAATCCAAAGACATCAATCAATCTTTTAAAGTAACGG 857
QY 792 GTTTTTCATGTCATCTATACCTGAGCCAGACACATGGAACCTTTGAGGAAAGTT 851
DB 858 GTTTTTCATGTCATCTATACCTGAGCCAGACACATGGAACCTTTGAGGAAAGTT 917
QY 852 CTCAGATGTTTCATCTCTGGCTCTGAACTTCTATGAAGGGGTCTCTGAAGATCAATCCAGA 911
DB 918 CTCAGATGTTTCATCTCTGGCTCTGAACTTCTATGAAGGGGTCTCTGAAGATCAATCCAGA 977
QY 912 TCACAGATTAACCTGTTCCAACTCCTCGAGAGCTCTCTTTGATTTCTTTTCAAGAGGC 971

Db 978 TGACAGATTAACTGGTTCCTCCCACTCTGGAGAGCTCTTACTTTGATTCTTTTCAAGAGGC 1037
 Qy 972 CCAAAATTAAGAAAGACACGCTATGAAGGAAGAAACAGAGAGCCCAACAG 1023
 Db 1038 CCAAAATTAAGAAAGACACGCTATGAAGGAAGAAACAGAGAGCCCAACAG 1089

RESULT 10
 AA164248
 ID AA164248 standard; cDNA; 882 BP.
 XX
 AC AA164248;
 XX
 DT 08-MAR-2002 (first entry)
 XX
 DE Human kinase 14257 cDNA.
 XX

Protein kinase; enzyme; cytosolic; osteopathic; hepatotropic;
 anti-diabetic; neuroprotective; antiarthritic; dermatological;
 immunosuppressive; anti-inflammatory; antithyroid; antipsoriatic;
 ophthalmological; antiallergic; antiasthmatic; antiatherosclerotic;
 hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic;
 immunomodulator; analgesic; cellular proliferative disorder; cancer;
 acute lymphoblastic leukaemia; Hodgkin's disease;
 bone metabolism disorder; osteoporosis; immune system disorder;
 inflammatory; diabetes mellitus; osteoarthritis; asthma;
 cardiovascular disorder; hypertension; coronary artery disease;
 endothelial cell disorder; psoriasis; ss.

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..128
 FT /*tag= a
 FT 129..815
 FT /*tag= b
 FT /*product= "Protein kinase 14275"
 FT 816..882
 FT /*tag= c
 XX
 PN W0200179488-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 13-APR-2001; 2001WO-US012188.
 XX
 PR 13-APR-2000; 2000US-0196910P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Kapeller-Libermann R;
 XX
 PS WPI: 2002-034355/04.
 DR P-PSDB; AAG78547.
 XX
 PT New 14257 polypeptides (protein kinases), useful as diagnostic targets
 PT and therapeutic agents for controlling cellular proliferative and/or
 PT differentiative disorder, bone disorders, immune disorders and
 PT cardiovascular disorders.
 XX
 PS Claim 2; Fig 1A; 98pp; English.
 XX

The invention relates to an isolated 14257 polypeptide and nucleic acid
 encoding it. The 14257 protein is a protein kinase that acts as a
 modulating agent in regulating a variety of cellular processes, including
 cell proliferation, differentiation, growth and division. The activity of
 the protein of the invention may be described as; cytosolic; osteopathic
 ; hepatotropic; antidiabetic; neuroprotective; antiarthritic;
 dermatological; immunosuppressive; anti-inflammatory; antithyroid;
 antipsoriatic; ophthalmological; antiallergic; antiasthmatic;
 antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide;
 anorectic; metabolic; immunomodulator and analgesic. The protein of the

CC invention may act as a novel diagnostic target or therapeutic agent
 CC controlling certain disorders, for example kinase-associated or other
 CC 14257-associated disorders. These may include cellular proliferative
 CC disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's
 CC disease. Other disorders include bone metabolism disorders such as
 CC osteoporosis, disorders of the immune system, e.g. inflammatory,
 CC diabetes mellitus, osteoarthritis and asthma. Proteins of the invention
 CC may also be of use as therapeutic agents in cardiovascular disorders such
 CC as hypertension and coronary artery disease, and some endothelial cell
 CC disorders, including psoriasis. The current sequence represents a human
 CC kinase 14257 cDNA
 XX
 SQ Sequence 882 BP; 288 A; 150 C; 198 G; 245 T; 0 U; 1 Other;
 Query Match 61.9%; Score 644; DB 6; Length 882;
 Best Local Similarity 99.2%; Pred. No. 1.le-161;
 Matches 647; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATCGMAAGTATGAAAAATAGCTAGACCTGGAGAGGCTCTTATGGGTGTGATTCAAA 60
 Db 129 ATGGGAAAGTATGAAAAATAGCTAGACCTGGAGAGGCTCTTATGGGTGTGATTCAAA 188
 Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTAAAAAATTTGGAATCTGAAGAT 120
 Db 189 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTAAAAAATTTGGAATCTGAAGAT 248
 Qy 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db 249 GATCCTATTGTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 308
 Qy 181 CCAAACTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGAAATGCAATTTAGTTTTT 240
 Db 309 CCAAACTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGAAATGCAATTTAGTTTTT 368
 Qy 241 GAATACCTGTCATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 Db 369 GAATACCTGTCATCATGCACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 428
 Qy 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
 Db 429 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 488
 Qy 361 AACTGTATTTCAGAGATATATAACCTGAAAAATTTCTTAATACTAAGCAAGGAAATATC 420
 Db 489 AACTGTATTTCAGAGATATATAACCTGAAAAATTTCTTAATACTAAGCAAGGAAATATC 548
 Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATTCAGAGAGATGCTACACCGATTAT 480
 Db 549 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATTCAGAGAGATGCTACACCGATTAT 608
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTTTGTGGGAGATATCTCAGTATGTTCT 540
 Db 609 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTTTGTGGGAGATATCTCAGTATGTTCT 668
 Qy 541 TCAGTCGATATATGGGCTATTTGTTGTTTTCAGAGAGCTCTCTGACAGGCCAGCCACTG 600
 Db 669 TCAGTCGATATATGGGCTATTTGTTGTTTTCAGAGAGCTCTCTGACAGGCCAGCCACTG 728
 Qy 601 TGGCCTGGAATAATCAGATGTGGACCACTTTATCTGATAATCAGAACACTAG 652
 Db 729 TGGCCTGGAATAATCAGATGTGGACCACTTTATCTGATAATCAGAACACTAG 780

RESULT 11
 ADI40928
 ID ADI40928 standard; cDNA; 1429 BP.
 XX
 AC ADI40928;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human kinase and phosphatase KPP-41 encoding cDNA SEQ ID NO:94.
 XX

human; kinase and phosphatase; KPP; enzyme; cardiovascular;
 antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory;
 antiangiinal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive;
 antithyroid; dermatological; antidiabetic; nephrotropic; antigout;
 gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic;
 ophthalmological; antirheumatic; antiparkinsonian; nootropic;
 anticonvulsant; hepatotropic; CNS; antipsoriatic; haemostatic;
 cytostatic; antilipemic; antiparasitic; antihelminthic; antibacterial;
 virucide; protozoacide; fungicide; gene therapy; kinase modulator;
 phosphatase modulator; cardiovascular disease; immune system disorder;
 neurological disorder; growth and development disorder;
 cell proliferative disorder; infection; gene; ss.

Homo sapiens.
 Key Location/Qualifiers
 CDS 70..621
 /*tag= a
 /product= "kinase and phosphatase KPP-41"

WO2004009778-A2.

29-JAN-2004.

18-JUL-2003; 2003WO-US022650.

19-JUL-2002; 2002US-0397354P.

02-AUG-2002; 2002US-0400599P.

02-AUG-2002; 2002US-0400783P.

15-AUG-2002; 2002US-0404027P.

(INCY-) INCYTE CORP.

Hafalia AJA, Emerling BM, Kable AE, Richardson TW, Becha SD;
 Baughn MR, Tang YT, Lal PG, Lee SY, Griffin JA, Khare R;
 Elliott VS, Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tran UK;
 Gururajan R, Ding L, Marquis JP, Thornton MB, Forsythe IJ, Lee EA;
 Gietzen KJ, Runkumar J;
 WPI: 2004-132950/13.
 P-PSDB: ADI40875.

New human kinases and phosphatases, useful for diagnosing, treating or
 preventing atherosclerosis, hypertension, AIDS, allergy, multiple
 sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
 or hepatitis.

Claim 5; SEQ ID NO 94; 330pp; English.

The present sequence encodes a human kinase and phosphatase (KPP)
 protein. KPP sequences have cardiovascular, antiarteriosclerotic,
 hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV,
 antiallergic, antiasthmatic, immunosuppressive, antithyroid,
 dermatological, antidiabetic, nephrotropic, antigout, gastrointestinal,
 neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological,
 antirheumatic, antiparkinsonian, nootropic, anticonvulsant, hepatotropic,
 CNS, antipsoriatic, haemostatic, cytostatic, antilipemic, antiparasitic,
 antihelminthic, antibacterial, virucide, protozoacide and fungicide
 activities, and can be used in gene therapy, and as kinase modulators and
 phosphatase modulators. KPP proteins, polynucleotides, agonists and
 antagonists can be used for diagnosing, treating or preventing disorders
 associated with aberrant expression of KPP, such as cardiovascular
 diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris
 or congestive heart failure), immune system disorders (e.g. AIDS,
 allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis,
 osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,
 Sjogren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's
 disease, Parkinson's disease, Huntington's disease, dementia or
 epilepsy), disorders affecting growth and development (e.g. cirrhosis,
 hepatitis, mixed connective tissue disease, psoriasis or primary
 thrombocytopenia), cell proliferative disorders (e.g.

hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial,
 fungal, parasitic, protozoan or helminthic infections. The KPP and
 polynucleotides are also useful in assessing the effects of exogenous
 compounds on the expression of nucleic acids and kinases and
 phosphatases, or for facilitating the drug discovery process, including
 determination of efficacy, dosage, toxicity and pharmacology. The
 polynucleotides encoding KPP are useful for creating transgenic animals
 to model human disease.

Sequence 1429 BP; 466 A; 286 C; 294 G; 383 T; 0 U; 0 Other;

Query Match 58.0%; Score 604; DB 12; Length 1429;
 Best Local Similarity 75.6%; Pred. No. 6.5e-151;
 Matches 848; Conservative 0; Mismatches 175; Indels 99; Gaps 4;

QY 1 ATGGAAGATATGAAAAATAGCTAAGACTGGAGAGGGTCTTATGGGGTTGATTCAAA 60
 DB 70 ATGGAAGATATGAAAAATAGCTAAGACTGGAGAGGGTCTTATGGGGTTGATTCAAA 129
 QY 61 TGCAGAAACAAACCTCTGGAACAAGTAGTGTGTTAAAAAATTTGGAATCTGAAGAT 120
 DB 130 TGCAGAAACAAACCTCTGGAACAAGTAGTGTGTTAAAAAATTTGGAATCTGAAGAT 189
 QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
 DB 190 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 249
 QY 181 CCAATCTTTGTGAACCTCATCGAGGTGTTTTCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
 DB 250 CCAATCTTTGTGAACCTCATCGAGGTGTTTTCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 309
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCAAATGGAGTTGCTGAT 300
 DB 310 GAATCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCAAATGGAGTTGCTGAT 369
 QY 301 GGAGTGATCAAAAGCGTATATTGGCAAAACACTTCAAGCTCTTAAATTTCTGTATATACAT 360
 DB 370 GGAGTGATCAAAAGCGTATATTGGCAAAACACTTCAAGCTCTTAAATTTCTGTATATACAT 429
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTAATTAACTAAGCAAGAAATAATC 420
 DB 430 AACTGTATTACAGAGATATAAAACCTGAAATATTCTAATTAACTAAGCAAGAAATAATC 489
 QY 421 AAGATTGTGACTTCGGGTTTCACAAATTTCTGATTCCAGGAGATGCTTA----- 470
 DB 490 AAGATTGTGACTTCGGGTTTCACAAATTTCTGATTCCAGGAGATGCTTA----- 549
 QY 471 -----CACGATTATATGATGCTACGAGATGGTACCGAGCTCCTGAA 510
 DB 550 GCTCATCTCGAACTTCTGGCCTCAAGTGATCTTCCACCTCGCCTCCCAAAGTCTGGA 609
 QY 511 CTTCTTGTGGGAGATACCTAGTATGGTCTTCAGTCGATATATGGGCTA----- 559
 DB 610 TTACAAGTGTGAGCCACCGTCCCGAGAGATTTTTCAAACAATAACTACTGAGAGCTCA 669
 QY 560 -----TTGGTGTGTTTTCAGAGCTCCTGAGAGGCTC 729
 DB 670 CAAGATTGTTTGTAGTGGGAACAAATTCGAACAATTTCTGAGAACCATTCAGGAG 729
 QY 593 A-----GCCACTGGGCTGGAAATCAGATGTGGAGCAACCTTTATCTG 636
 DB 730 ATGCTCATACACCGATTGTGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAG 789
 QY 637 ATAATCAGAACACTAGTAGAGCG-----GGGTTTGGCACTGTTGACCAAG 681
 DB 790 ATACTCAGTATGGTTCCTCAGTCGATATGGGCTATGTTGTTTGTGACAGAGCTCCTG 849
 QY 682 GCTGCTCGAACTCTTACAGCTCAAGTATCCACCTGCGGTAGCTCTCAAGAGTCTGGA 741
 DB 850 ACAGCCAGCCACTGTGGCTTGGAAATCAGATGTGGAGCAACCTTTATCTGATATCAGA 909
 QY 742 ATTACAGGAAATTAATCCAGAGCATCAATCAATCTTTAAAGTAACGGGTTTTCCAT 801

Db 910 A C A C T A G G A A A T T A A T C C C A G A C A T C A A T C T T T A A A A G T A A C G G T T T T C C A T 969
 Qy 802 G G C A T C A G T A T A C T G A G C C A G A A G A C A T G G A A A C T C T T G A G G A A A G T T C T C A G A T G T T 861
 Db 970 G G C A T C A G T A T A C T G A G C C A G A A G A C A T G G A A A C T C T T G A G G A A A G T T C T C A G A T G T T 1029
 Qy 862 C A T C T G T G C T C T G A A C T T C A T G A A G G G T G T C T G A A G A T G A T C C A G A T C A G A T T A 921
 Db 1030 C A T C T G T G C T C T G A A C T T C A T G A A G G G T G T C T G A A G A T G A T C C A G A T C A G A T T A 1089
 Qy 922 A C T G T T C C C A A C T C C T G G A G A G C T C T A C T T T G A T T C T T T C A A G A G G C C A A A T T A A A 981
 Db 1090 A C T G T T C C C A A C T C C T G G A G A G C T C T A C T T T G A T T C T T T C A A G A G G C C A A A T T A A A 1149
 Qy 982 A G A A A A C A C G T A A T G A A G G A A A A C A G A A G C C A A C A G 1023
 Db 1150 A G A A A A C A C G T A A T G A A G G A A A A C A G A A G A G C C A A C A G 1191

RESULT 12
 ABX34679
 ID ABX34679 standard; cDNA; 1281 BP.
 AC ABX34679;
 XX
 DT 13-FEB-2003 (first entry)
 XX
 DE Human mddt cDNA SEQ ID 240.
 XX
 KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianemic; antiproliferative; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
 KW psoriasis; hepatitis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-US009944.
 XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tudson O, Yap PE, Amshay SR;
 PI Daugherty SC, Lam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 XX WPI; 2003-058431/05.
 DR P-PSDB; ABU11689.
 DR
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 XX Claim 1; SEQ ID NO 240; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianemic, antiproliferative and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukemia, lymphoma, melanoma, myeloma or sarcoma), Goodpasture's
 CC disease, acquired immunodeficiency syndrome (AIDS), anaemia, Crohn's
 CC syndromes, inflammation, osteoporosis, thrombocytopenia, psoriasis or
 CC hepatitis. ABX3440-ABX34835 encode the MDDT polypeptides represented in
 CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Seq Sequence 1281 BP; 428 A; 191 C; 317 G; 345 T; 0 U; 0 Other;
 Query Match 52.2%; Score 543.2; DB 8; Length 1281;
 Best Local Similarity 99.5%; Pred. No. 1.1e-134;
 Matches 545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 A T G G A A A G T A T G A A A A A T T A G C T A A C A C T G G A G A G G T C T T A T G G G T T G T A T T C A A A 60
 Db 704 A T G G A A A G T A T G A A A A A T T A G C T A A C A C T G G A G A G G T C T T A T G G G T T G T A T T C A A A 763
 Qy 61 T G C A G A A C A A A A C C T C T G C A C A G T A G T A G C T T T A A A A A T T G G G A T C T G A A G A T 120
 Db 764 T G C A G A A C A A A A C C T C T G C A C A G T A G T A G C T T T A A A A A T T G G G A T C T G A A G A T 823
 Qy 121 G A T C C T C T T G T T A G A A A A T A G C A C T A A G A G A A T A C G T A T G T T G A A G C A A T T A A A A C A T 180
 Db 824 G A T C C T C T T G T T A G A A A A T A G C A C T A A G A G A A T A C G T A T G T T G A A G C A A T T A A A C A T 883
 Qy 181 C C A A A T C T T G T G A A C C T C A T C G A G G T G T T C A G G A G A A A A A G A A A A T G C A T T A G T T T T T 240
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 Qy 241 G A A T A C T G T C A T C A T A C A C A C T T T T A A A T G A G T G G A A A G A A C C C A A A T G G A T T G C T G A T 300
 Db 944 G A A T A C T G T C A T C A T A C A C A C T T T T A A A T G G G C T G G A A A A A C C C A A A T G G A T T G C T G A T 1003
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 Qy 541 T C A G T C G A 548
 Db 1244 T C A G T C A A 1251

RESULT 13
 AAF44669
 ID AAF44669 standard; cDNA; 911 BP.
 XX
 AC AAF44669;
 XX
 DT 27-MAR-2001 (first entry)

XX DE Novel protein kinase cDNA, SEQ ID NO: 49.
 XX KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX OS Homo sapiens.
 XX WO2000073469-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US014842.
 XX PR 28-MAY-1999; 99US-0136503P.
 XX PA (SUGEN-) SUGEN INC.
 XX PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
 DR WPI; 2001-032161/04.
 DR P-PSDB; AAB65642.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 XX Example 4; Fig 2; 310pp; English.
 XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 CC stress related disorders, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
 CC disorders
 XX SQ Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;
 Query Match 51.6%; Score 537; DB 4; Length 911;
 Best Local Similarity 87.0%; Pred.No. 4.4e-133;
 Matches 643; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 XX 285 AATGGAGTGTGGTGGAGTGTATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAA 344
 1. AATGGAGTGTGGTGGAGTGTATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAA 60
 XX 345 TTCTCTCATATACATCACTGTATTCACAGAGATATAAAACCTGAAATATTTCTAATAAC 404
 61 TTCTCTCATATACATCACTGTATTCACAGAGATATAAAACCTGAAATATTTCTAATAAC 120
 XX 405 TAAGCAAGGAATTAATCAAGATTTGTGACTTCGGGTTTGACAAATTCGATTTCCAGGAGA 464
 121 TAAGCAAGGAATTAATCAAGATTTGTGACTTCGGGTTTGACAAATTCGATTTCCAGGAGA 180
 XX 465 TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAATCTTTGTGGAGA 524
 181 TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAATCTTTGTGGAGA 240

QY 525 TACTCAGTATGGTCTTCTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCCT 584
 Db 241 TACTCAGTATGGTCTTCTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCCT 300
 QY 585 GACAGGCCAGCCACTGTGGCTCTGAAATCAGATGTGACCAACTTTTATCTGATAATCAG 644
 Db 301 GACAGGCCAGCCACTGTGGCTCTGAAATCAGATGTGACCAACTTTTATCTGATAATCAG 360
 QY 645 AAGACTAGTAGAGACGGGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGTC 704
 Db 361 AACACT----- 366
 QY 705 AAGTGATCCACCTGCCGTAGCCTCTCAAAGTCTGGAAATTACAGGAAATTAATCCCAAG 764
 Db 367 -----AGGAAATTAATCCCAAG 384
 QY 765 ACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTCAGGCCAGA 824
 Db 385 ACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTCAGGCCAGA 444
 QY 825 AGACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAATTCAT 884
 Db 445 AGACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAATTCAT 504
 QY 885 GAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCACTCTCGAGAG 944
 Db 505 GAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCACTCTCGAGAG 564
 QY 945 CTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGAACGTAATGAAGGAAG 1004
 Db 565 CTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGAACGTAATGAAGGAAG 624
 QY 1005 AACAGAGACGCCCAACAG 1023
 Db 625 AACAGAGACGCCCAACAG 643
 RESULT 14
 ADI29367
 ID ADI29367 standard; cDNA; 911 BP.
 XX AC ADI29367;
 XX DT 22-APR-2004 (first entry)
 XX Human MARK3-associated cDNA #37.
 KW Human; ss; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX OS Homo sapiens.
 XX US2003232771-A1.
 XX PD 18-DEC-2003.
 XX PF 17-JUN-2002; 2002US-00174319.
 XX PR 17-JUN-2002; 2002US-00174319.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Ward DT, Freier SM, Dobie KW;
 DR WPI; 2004-052188/05.
 DR P-PSDB; ADI29249.
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.

PS Disclosure; Fig 2; 233pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80
 CC base pairs (bp) targeted to a nucleic acid encoding MARK3
 CC (MAP/microtubule affinity-regulating kinase 3), that specifically
 CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
 CC composition comprising the compound and a carrier or diluent, inhibiting
 CC the expression of MARK3 in cells or tissues, treating an animal having or
 CC suspected of having a disease or condition associated with MARK3 and
 CC screening for an antisense compound. The antisense oligonucleotide is
 CC useful for preparing a composition for treating hyperproliferative
 CC disorder, particularly cancer and neurodegenerative diseases e.g.
 CC Alzheimer's disease. The present sequence is a MARK3 associated cDNA
 CC included in the figures but not mentioned anywhere else in the
 CC specification.

XX Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;

SQ Query Match 51.6%; Score 537; DB 12; Length 911;
 Best Local Similarity 87.0%; Pred. No. 4.4e-133;
 Matches 643; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 285 AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGCGAACACCTTCAAGCTCTTAA 344
 DB 1 AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGCGAACACCTTCAAGCTCTTAA 60

QY 345 TTCTCTCATATACATAACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATAAC 404
 DB 61 TTCTCTCATATACATAACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATAAC 120

QY 405 TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGA 464
 DB 121 TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGA 180

QY 465 TGCTACACCGATTATAGTACGATGGTACCGAGCTCCTGAACTTTTGTGGGAGA 524
 DB 181 TGCTACACCGATTATAGTACGATGGTACCGAGCTCCTGAACTTTTGTGGGAGA 240

QY 525 TACTCAGTATGTTCTTCAGTCGATATATGGCTTATGGTGTGTTTGTGACAGAGCTCCT 584
 DB 241 TACTCAGTATGTTCTTCAGTCGATATATGGCTTATGGTGTGTTTGTGACAGAGCTCCT 300

QY 585 GACAGGCCAGCACTGTGGCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 644
 DB 301 GACAGGCCAGCACTGTGGCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 360

QY 645 AACACTAGTAGAGAGCGGGTTTCCCAATGTTGACAGGCTGGTCTCGAACTCTTGACGTC 704
 DB 361 AACACT-----

QY 705 AAGTGATCCACCTGCGCTAGCCTCTCAAAGTGTGGAATTACAGGAAATTAATCCCAAG 764
 DB 367 -----AGGAAATTAATCCCAAG 384

QY 765 ACATCAATCAATCTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 824
 DB 385 ACATCAATCAATCTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 444

QY 825 AGACATGGAACCTTCAGGAAAGTGTCTCAGATGTTTCATCTGTGGCTCTGAACCTTCAT 884
 DB 445 AGACATGGAACCTTCAGGAAAGTGTCTCAGATGTTTCATCTGTGGCTCTGAACCTTCAT 504

QY 885 GAAGGGGTGTCTGAAGATGAATCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAG 944
 DB 505 GAAGGGGTGTCTGAAGATGAATCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAG 564

QY 945 CTCCTACTTTGATTTCTTTTCAAGAGGCGCCAAATTAAGAAAGAAAGCAAGTAAAGGAAG 1004
 DB 565 CTCCTACTTTGATTTCTTTTCAAGAGGCGCCAAATTAAGAAAGAAAGCAAGTAAAGGAAG 624

QY 1005 AACAGAGAGCGCAACAG 1023.

Db 625 AACAGAGAGCGCAACAG 643

RESULT 15

AAAD03812

ID AAD03812 standard; cDNA; 561 BP.

XX AAD03812;

DT 19-JUN-2001 (first entry)

DE Human kinase cDNA #1.

XX Human; kinase; gene therapy; bioreactor; mental disorder;

KW biological disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..561

FT /tag= a

FT /product= "Human kinase #1"

FT /note= "The coding region does not include stop codon"

FT /partial

XX W0200123579-A1.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026621.

XX 28-SEP-1999; 99US-0156511P.

XX (LEXI-) LEXICON GENETICS INC.

XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;

PI Sands AT;

XX WPI; 2001-266166/27.

DR P-PSDB; AAE00490.

XX New isolated human kinase polynucleotide useful for generating for

PT antibodies, as reagents in diagnostic assays and for screening for

PT compounds useful for treating mental, biological or medical diseases.

XX Disclosure; Page 27; 38pp; English.

XX The present sequence is a cDNA encoding novel human protein (NHP) known

CC as human kinase. The human kinases share structural similarity with

CC animal kinases, more particularly serine or threonine protein kinases.

CC Human kinase cDNA is useful for the detection of mutant human kinase for

CC the diagnosis of disease, and also as a therapeutic. It is useful for

CC screening drugs effective in the treatment of symptomatic or phenotypic

CC manifestations perturbing the normal function of NHP in the body. The NHP

CC nucleotide sequences are useful for generation of antibodies, as reagents

CC in diagnostic assays, for the identification of other cellular gene

CC products related to human kinases, and as reagents in assays for

CC screening compounds that are useful for treating mental, biological or

CC medical disorders. NHP oligonucleotides are used as probes. The labelled

CC NHP probes are useful for screening human genomic library for identifying

CC polymorphisms and as primers in amplification assays to detect mutations

CC within the exons, introns and splice sites that can be used in

CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP

CC products are used to genetically engineer cells in vivo that functions as

CC bioreactors in the body delivering a continuous supply of NHP to the

CC body. Nucleotide constructs encoding functional NHPs are used in gene

CC therapy for the modulation of NHP expression

XX SQ Sequence 561 BP; 189 A; 87 C; 112 G; 173 T; 0 U; 0 Other;

Query Match 43.7%; Score 454.4; DB 4; Length 561;
 Best Local Similarity 99.8%; Pred. No. 4.3e-111;
 Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	121	GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT	180
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Qy	181	CCAAATCTTGTGAACCTCATCGAGGTGTTCAAGGAGAAAAAGGAAATGCAATTTAGTTTTT	240
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Qy	301	GGAGTGATCAAAAGCGTATTATGCGAACACCTTCAAGCTCTTAATTTCTGCATATACAT	360
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Qy	361	AACGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATATC	420
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:25:49 ; Search time 4527.25 Seconds
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Perfect score: 1041

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: gb_ov.*
6: gb_pat.*
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12: gb_sy.*
13: gb_un.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	762.8	73.3	1678	6 AX698820	Sequence
11	757	72.7	1083	6 AX166534	Sequence
12	709	68.1	1819	6 AR492171	Sequence
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16	537	51.6	911	6 AX056404	Sequence
17	454.4	43.7	561	6 AR492165	Sequence
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ALIGNMENTS

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DEFINITION Sequence 9 from patent US 6716616.
ACCESSION AR492169
VERSION AR492169.1 GI:47260679
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1041)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 9 06-APR-2004;
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DEFINITION Sequence 9 from Patent WO0123579.
ACCESSION AX107720
VERSION AX107720.1 GI:13923201
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 9 05-APR-2001;
Lexicon Genetics Incorporated (US)

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DEFINITION Sequence 3 from patent US 6716616.
ACCESSION AR492166
VERSION AR492166.1 GI:47260676
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 3 06-APR-2004;
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DEFINITION Sequence 3 from Patent WO0123579.
ACCESSION AX107714
VERSION AX107714.1 GI:13923198
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 3 05-APR-2001;
Lexicon Genetics Incorporated (US)
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2e-239;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION AR492170
ACCESSION AR492170
VERSION AR492170.1
KEYWORDS GI:47260680
SOURCE Unknown.
ORGANISM Unknown.

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Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
Human kinase proteins and polynucleotides encoding the same
Patent: US 6716616-A 11 06-APR-2004;
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Best Local Similarity 90.8%; Pred. No. 5.1e-194;
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LOCUS
DEFINITION Sequence 11 from Patent WO0123579.
ACCESSION AX107722
VERSION AX107722.1 GI:13923202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 11 05-APR-2001;
Lexicon Genetics Incorporated (US)
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ORIGIN
Query Match 80.6%; Score 839; DB 6; Length 945;
Best Local Similarity 90.6%; Pred. No. 5.1e-194;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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LOCUS
DEFINITION Sequence 5 from patent US 6716616.
ACCESSION AR492167
VERSION AR492167.1 GI:47260677
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 972)
AUTHORS Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B.
and Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 5 05-APR-2004;
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 79.1%; Score 823; DB 6; Length 972;
Best Local Similarity 90.6%; Pred. No. 4.1e-190;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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RESULT 8
AX107716
LOCUS
DEFINITION

Sequence 5 from Patent WO0123579. 972 bp DNA linear PAT 30-APR-2001

AX107716
AX107716.1 GI:13923199
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Doncho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
Human kinase proteins and polynucleotides encoding the same
Patent: WO 0123579-A 5 05-APR-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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source
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ORIGIN

Query Match 79.1%; Score 823; DB 6; Length 972;
Best Local Similarity 90.6%; Pred. No. 4.1e-190;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 1 ATGGAAGCTATGAAAATTTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTTATTCAAA 60
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Db 925 CAGGT 929

RESULT 9
AX746179 1790 bp DNA linear PAT 13-JUN-2003
LOCUS
DEFINITION Sequence 30 from Patent WO0208399.
ACCESSION AX746179
VERSION AX746179.1 GI:31746165
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Yue, H., Khan, F.A., Gururajan, R., Hafalia, A.J., Chawla, N.K.,
Arvizu, C.S., Ramesh, J., Gandhi, A.R., Policky, J.L., Baughn, M.R.,
Tribouley, C.M., Bandman, O., Nguyen, D.B., Lu, Y., Burford, N., Lal, P.,
Ding, L., Yao, M.G., Elliott, V.S., Recipon, S.A., Kearney, L., Lu, D.A.,
Greenwald, S.R., Tang, Y.T., Xu, Y., Walsh, R.T., Gietzen, K.J.,
Yang, J., Jackson, J.L. and Thornton, M.
HUMAN KINASES
TITLE Human kinases
JOURNAL Patent: WO 0208399-A 30 31-JAN-2002;
Incyte Genomics, Inc. (US); Thornton, Michael (US)
FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 1698381CB1"

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Query Match 78.9%; Score 821; DB 6; Length 1790;
Best Local Similarity 90.6%; Pred. No. 1.3e-169;
Matches 927; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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Qy 1021 CAG 1023
Db 1163 CAG 1165

RESULT 10
AX698820 1678 bp DNA linear PAT 02-APR-2003
LOCUS
DEFINITION Sequence 6 from Patent WO02079473.
ACCESSION AX698820
VERSION AX698820.1 GI:29499608
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Panzer, S.R., Lincoln, S.E., Altus, C.M., Dufour, G.E., Hillman, J.L.,
Jones, A.L., Dam, T.C., Liu, T.F., Harris, B., Flores, V., Daffo, A.,
Marwaha, R., Chen, A.J., Chang, S.C., Gerstin, J.E., Peralta, C.H.,
David, M.H. and Lewis, S.A.
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TITLE Molecules for diagnostics and therapeutics
JOURNAL Patent: WO 0209473-A 6 10-OCT-2002;
Incyte Genomics, Inc. (US)

FEATURES
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1. 1678
Location/Qualifiers
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ORIGIN

Query Match 73.3%; Score 762.8; DB 6; Length 1678;
Best Local Similarity 90.0%; Pred. No. 2e-175;
Matches 925; Conservative 0; Mismatches 2; Indels 101; Gaps 6;

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DB |||||

RESULT 11
AX166534
LOCUS
DEFINITION Sequence 25 from Patent WO0138503.
ACCESSION AX166534
VERSION AX166534.1 GI:14546879
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
Flanagan, P. and Clary, D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 25 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
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Best Local Similarity 86.1%; Pred. No. 5.1e-174;
Matches 927; Conservative 0; Mismatches 0; Indels 150; Gaps 2;

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LOCUS 1819 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 13 from patent US 6716616.
ACCESSION AR492171
VERSION AR492171.1 GI:47260681
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1819)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 13 06-APR-2004;
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Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

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LOCUS
DEFINITION Sequence 13 from Patent WO0123579.
ACCESSION AX107724
VERSION AX107724.1 GI:13923203
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 13 05-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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Query Match 68.1%; Score 709; DB 6; Length 1819;
Best Local Similarity 77.0%; Pred. No. 2.6e-162;
Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

QY 1 ATGGAAGAAGTATGAAAATTTAGCTAAGACTGGAGAAGGGCTTATGGGGTTGATTCAAA 60
Db 138 ATGGAAGAAGTATGAAAATTTAGCTAAGACTGGAGAAGGGCTTATGGGGTTGATTCAAA 197
QY 61 TGCAGAAACAAACCTCTGCAACAGTAGTAGCTGTTAAAAAATTTGTTGGAATCTGAAGAT 120
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LOCUS
DEFINITION Sequence 3 from Patent WO0179488.
ACCESSION AX286069
VERSION AX286069.1 GI:17045995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE	1	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	Kapeller-Libermann, R.	
TITLE	14257, protein kinase molecules and uses therefor	
JOURNAL	Patent: WO 0179488-A 1 25-OCT-2001;	
FEATURES	Millennium Pharmaceuticals, Inc. (US)	
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DEFINITION	Sequence 1 from Patent WO0179488.	
ACCESSION	AX286067	
VERSION	AX286067.1	GI:17045993
KEYWORDS		
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	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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DEFINITION
ACCESSION CB169554
VERSION CB169554.1 GI:28155681
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 695)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
ADDITIONAL INFORMATION: Adelson, D.L. and Gill, C.A.
TITLE Bovine ESTs (Adelson and Gill)
JOURNAL Unpublished (2003)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.

FEATURES
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QY 541 TCA 543
Db 3 TCA 1

RESULT 2
BY733578
LOCUS
DEFINITION
BY733578 670 bp mRNA linear EST 17-DEC-2002
diencephalon Mus musculus cDNA clone G630052E12 5', mRNA sequence.
BY733578
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 670)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,K., I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojohori,T., Baldarelli,R., Hill,D.P., Buit,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,D.A., Bradt,D., Brusica,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Redziarski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L.G., Wainwright,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

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TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sphiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resescg.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hayashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
Location/Qualifiers
source
1..670
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G630052E12"
/sex="male"
/tissue_type="diencephalon"
/dev_stage="16 days neonate"
/clone_lib="RIKEN full-length enriched, 16 days neonate
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Best Local Similarity 85.6%; Pred. No. 3.5e-92;
Matches 450; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 1 ATGGAAGATATGAAATATAGTCTAGAGTGGAGAGGCTTATGGGGTTGTTATTCAAA 60
Db 145 ATGGAAGATATGAAATATAGTCTAGAGTGGAGAGGCTTATGGGGTTGTTATTCAAA 204
QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 205 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 264
QY 121 GATCTGTTGTAGAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACACAT 180
Db 265 GATCTGTTGTAGAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACACAT 324

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Qy	181	CCAAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCATTAGTTTT	240
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Qy	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCAAATGAGTTGCTGAT	300
Db	385	GAGTACTGTGATCATACACTTTTAAACGAGCTGGAGAAACCCAAACGAGTTTCTGAT	444
Qy	301	GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
Db	445	GGAGTGATTAAGAGTGTCTATGGCAACCCCTTCAAGCCCTTAACTTCTGTCAACAGCAC	504
Qy	361	AACGTGATTCACAGAGATATAAACCTGAAATATTTCTAATACTAAGCAGGAATATC	420
Db	505	AATGTGATTCACAGAGATATAAACCTGAAATATTTCTAATACTAAGCAGGAATATC	564
Qy	421	AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGGAGATGCTTACACCGATTAT	480
Db	565	AAGATTTGTGACTTCGGGTTTGCAGGAATTTCTAATTCAGGAGATGCTTACACGACTAT	624
Qy	481	GTAGCTACGAGATGATACCGAGCTCTGAACTTCTTGTGGAGATA	526
Db	625	GTTGCCACAGGTGTGATCCGAGCCGCAACTTCTGCGGGAGACA	670
RESULT 3			
AK016781			
LOCUS			
DEFINITION			
ACCSSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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177 ATGGAATAATGAAAAATGGAAGATTGGAAGGCTCTATGGGTAGTGTCAAG 236
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897 CCAGACCTTGAAGACATGGAACACTTGGATTGAAATTTCCAAACATCTCTACTCTGCA 956
778 CTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATCAGATTAACCTGTTCCTCAA 837
957 CTGGCTCTTAAAGGCTGCTCCATGATGATCTCTGAGAGGCTGATCGGAACAG 1016
838 CTCCTGAGAGCTCTCTACTTTGATTTCTTTTCAAGAGG 874
1017 CTGTTGAGCATCCATATTTTGACAGCATTCGAGAAG 1053

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RESULT 4
CB315094
LOCUS
DEFINITION
  CB315094 825 bp mRNA linear EST 04-MAR-2003
  IMAGE:6888377 5', mRNA sequence.
ACCESSION
  CB315094
VERSION
  CB315094.1 GI:28838974
KEYWORDS
  EST.
SOURCE
  Rattus norvegicus (Norway rat)
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.

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1 (bases 1 to 825)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-i@mail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L10M3144 row: i column: 16
High quality sequence stop: 468.
FEATURES
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            /db_xref="taxon:10116"
            /clone="IMAGE:6888377"
            /tissue_type="Pituitary"
            /lab_host="DH10B"
            /clone_lib="NICHD Rr Pit1"
            /notes="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; 5'
            and 3' adaptors were used in cloning as follows: 5'
            adaptor sequence: 5'-ATCTAGAGCCGAGGCGCCGACATG-dt(30)BN-3'
            (where B = A, C, G, or T). Average
            insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, CA)."
ORIGIN
    Query Match 41.3%; Score 390.6; DB 6; Length 825;
    Best Local Similarity 83.3%; Pred. No. 1.7e-88;
    Matches 455; Conservative 0; Mismatches 90; Indels 1; Gaps 1;
    QY 361 AACTGTATTCACAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
    Db 96 AGCTGTATTCATCGGACCGTAAACCCGAAACATCTTAATAGCCAAGCAAGGTGATA 155
    QY 421 AAGATTTGTGACTTCTGGGTTTGCACAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
    Db 156 AAGATTTGTGACTTCTGGGTTTGCACAAATTTCTGATTCAGAGATGCTTACACAGACTAT 215
    QY 481 GTAGCTACGAGATGGTACCGAGCTCTCGAACTTTCTTGTGGAGATATCTCAGTATGTTCT 540
    Db 216 GTTGCCACCGAGGTGTACCGAGCCCTGAACTTTCTTGTGGAGACACGAAGTACGGCTCC 275
    QY 541 TCGTGTGATATATGGGCTATTTGTTGTTTTCAGAGCTCTGACAGGCTCTGACAGCCAGCCACTG 600
    Db 276 TCTGTGACATATATGGGCTGTGCGCTGTGTTTTCAGAGCTCTGACCGCTCAGCCACTC 335
    QY 601 TGGCTTGGAAATTCAGATGTGACCAACTTTATCTGATATCAAGACACTTAGGAAATTA 660
    Db 336 TGGCCAGGAAATTCAGATGTGACCAACTTTATCTGATCATCAGGACATTTGGAAAGCTG 395
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    Db 396 ATCCCAAGGACATCAGTCTATCTTTAAAGTAAGCAAGTATTTTCGTTGGCATCAGCATACC 455
    QY 721 GAGCCAGAGACATGGAACCTCTTGGAGAAAGTTCTCAGATGTTTCATCTCTGGGCTCTG 780
    Db 456 GAACCTGAGGACATGAGACTCTTGAAGAAATTTCTCAAAATGTTTCAGGCTATGGCTTTA 515
    QY 781 AACTTTCATG- AAGGGGTGTCTGAAGATGAATCAGATGACAGATTAACCTGTTCCTCAACT 839
    Db 516 AGTTTCATGAAGAGGTGTCTGAAGATGATCCTGATGAGAGGCTGACCTGTGCCAGCT 575
    QY 840 CTGGAGAGCTCTCTACTTGTGATTTCTTTTCAAGAGGCCCAATTTAAAGAAAGACGATAA 899

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Db      576 GTTGACAGTACTTCTCGAGTCTTTTCAAGAGACCAATGAAAGAAAGCCGCCGAA 635
Qy      900 TGAAGG 905
Db      636 TGAGGG 641

RESULT 5
BU686325/c
LOCUS   BU686325      536 bp      mRNA      linear      EST 07-OCT-2002
DEFINITION
UI-CF-DUI-adn-i-10-0-UI.s1 UI-CF-DUI Homo sapiens cDNA clone
UI-CF-DUI-adn-i-10-0-UI 3', mRNA sequence.
ACCESSION
BU686325
VERSION
BU686325.1 GI:23541120
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 536)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Genetics (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
1. 536
/organism="Homo sapiens"
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/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-DUI is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCGCTGAGGC.
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG LIB=UI-CF-DUI
TAG_SEQ=GGCTGAGGC"

FEATURES
source
1. 536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-DUI-adn-i-10-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-DUI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-DUI is a normalized cDNA library containing the
following tissue(s): Primary Lung Epithelial Cells The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT73-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCGCTGAGGC.

ORIGIN
Query Match 38.2%; Score 361; DB 5; Length 536;

TITLE
Analysis of the mouse transcriptome based on functional annotation

```

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Best Local Similarity 100.0%; Pred. No. 5.5e-81;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      585 GACAGGCCAGCCACTGTGGCTGTGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 644
      ||| |||
Db      536 GACAGGCCAGCCACTGTGGCTGTGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 477

Qy      645 AACACTAGGAAAATTAATCCAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA 704
      ||| |||
Db      476 AACACTAGGAAAATTAATCCAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA 417

Qy      705 TGGCATCAGTATACCTCGAGCAGACATGGAACCTCTTGAGGAAAGTTCTCAGATGT 764
      ||| |||
Db      416 TGGCATCAGTATACCTCGAGCAGACATGGAACCTCTTGAGGAAAGTTCTCAGATGT 357

Qy      765 TCATCTCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 824
      ||| |||
Db      356 TCATCTCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 297

Qy      825 AACCTGTGTCACACTCTCGAGAGCTCTTACTTTTGATCTTTTCAAGAGGCCCAATTA 884
      ||| |||
Db      296 AACCTGTGTCACACTCTCGAGAGCTCTTACTTTTGATCTTTTCAAGAGGCCCAATTA 237

Qy      885 AAGAAAGCAGCTTAATGAAGGAAGAACAGACGCGCAACAGCTACTTCGCTCAAAAG 944
      ||| |||
Db      236 AAGAAAGCAGCTTAATGAAGGAAGAACAGACGCGCAACAGCTACTTCGCTCAAAAG 177

Qy      945 T 945
      |
Db      176 T 176

```

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RESULT 6
BY752739      689 bp      mRNA      linear      EST 17-DEC-2002
LOCUS   BY752739      RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION
BY752739      RIKEN full-length enriched, adult inner ear Mus musculus
ACCESSION
BY752739.1 GI:27183802
VERSION
BY752739.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 689)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godik,A., Gough,J., Grimond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawai,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Kongaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Perte,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynehaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,J., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayashizumi,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,B. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation

```


ORIGIN

Query Match	35.3%;	Score 333.6;	DB 1;	Length 500;
Best Local Similarity	82.3%;	Pred. No. 5.3e-74;		
Matches 408;	Conservative 0;	Mismatches 84;	Indels 4;	Gaps 2;
QY	135	GAATAATGACCTAAGAGAAATACCTATCTGTGAAGCAATTAAACCATTTAAACATCCAAATCTGTGAA	194	
DB	2	GAATAATAGCCCTGCGGAAATCCGTATGCTGAAG---TTGAACACACCCAAACCTCGTGA	58	
QY	195	CCTCATCGAGGTGTTTCAGGAGAAAAGGAAATGCAATTAGTCTTTTGAATACTGTGATCA	254	
DB	59	CCTCATCGAGGTGTTTCAGAGAAAGAAAGATGCACTAGTCTTTTGAGTACTGTGATCA	118	
QY	255	TACACTTTTAAATGAGCTGGAGAAACCCAAATGGAGTTCTCTGATGGAGTGATCAAAAG	314	
DB	119	CACACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTTAAAG	178	
QY	315	CGTATTATGCAACACATCTCAAGCTCTTAATTTCTGTCATATACATAACTGATTTTCACAG	374	
DB	179	TGTGCTATGGAAACCCCTTCAAGCCCTTAACTCTGTGCACAGCACCAATTTGATTTCAATCG	238	
QY	375	AGATATAAAACCTGAAAATAATTTCTAATAACTAAGCAAGGAATAATCAAGATTTGTGACTT	434	
DB	239	GGATGTAACACCTGAAACATCTTAATAACCAAGCAAGGATGATAAGATTTGTGACTT	298	
QY	435	CGGTTTGGCAAAATTCGATTCAGAGATGCTTACACCGATTTATGTAGCTACGAGATG	494	
DB	299	TGGATTTGCAAGAAATCTAAATTCAGGAGACGCCATACAGACTATGTTGCCACCGGTG	358	
QY	495	GTACCGAGCTCCTGAACCTTTGTGGGAGATACCTCAGTATGGTTCTTCAGTTCGATATATG	554	
DB	359	GTACCGAGCCCTCGAACTTCTTCGTTGGGAGACACGAAGTACGGTTCTCTGTAGACGTGTG	418	
QY	555	GGCTATTGGTGTGTTTTTTCAGAGCTCCTTGACAGGCCAGGCCACTGTGGCCCTGGAAATC	614	
DB	419	GGCCGTGGCTGTGTTTATGCAGAGCTTCTGACGTGTGAGCCACTCTGGCCCGG-AAATA	477	
QY	615	AGATGTGGACCAACTT	630	
DB	478	CGACGTGGACCACTT	493	

RESULT 8				
BU221831				
LOCUS	824 bp	mRNA	linear	EST 25-NOV-2002
DEFINITION	BU221831	603750354F1	CSEQCHN04 Gallus gallus CDNA clone CHEST661113 5', mRNA sequence.	

ACCESSION	BU221831
VERSION	BU221831.1
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus

REFERENCE	1 (bases 1 to 824)
AUTHORS	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE	A Comprehensive Collection of Chicken cDNAs
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE	22335534
PUBMED	12445392
COMMENT	Contact: Simon Hubbard

Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..824

[illegible]

ORIGIN

Query Match	33.8%;	Score 319.4;	DB 5;	Length 824;
Best Local Similarity	67.2%;	Pred. No. 2.4e-70;		
Matches 483;	Conservative	0;	Mismatches 231;	
			Indels 5;	Gaps 2;

Qy		40	TCTTATGGGGTTGTATTC	AAATGTCAGAGAAACAA	AAACCTCTCGACAAGTAGTAGCTGT	TATAA	99	
Db		2	TCCTACGGCGTCGTCT	CAAGTCGCGCAACAGGAGAG	CGGGCGAGATCGTGGCCATCAAG		61	
Qy		100	AAATTTGTGGAATCTG	AAAGATGATCCTGTTGTT	TAAAGAAAATAGCACATAAGAGAAATACGT		159	
Db		62	AAGTTCCTGGAGTCCG	AGGAGGACCCGGTGAT	CCGGAAGATCGCGCTGCGGAGGTCGCG		121	
Qy		160	ATGTTGAAGCAATTTAA	AACATCCAAATCTTGT	GAAACCTCATCGAGGTGTT	CAGGAGAAA	219	
Db		122	ATGCTGAAGCAACTG	RAAACACCCCAACCT	GGTGAACCTGCTGGAGGTGTT	CAGGAGAAAG	181	
Qy		220	AGGAAATGCAATTTAG	TTTTTGGTAATCTGTG	TATCATACATCTTTAAAT	GAGCTGGAAGA	279	
Db		182	AGGAAGCTGCACCTG	GTCTTTTGATGCTGTG	ACACACCGTCTCCACGAGCTGGA	CAAG	241	
Qy		280	AAACCAATGGAGTGT	GTGATGGAGTGATCAA	AAAGCGTATTATGGCAAAACATTTCAAGCT		339	
Db		242	CACCCCGGGGTCCG	AGAGAGCTGGTCAG	AGCAATTACCTGGCAGACCTTCCAAACT		301	
Qy		340	CTTAAATTTGTGCAT	ATACATAAATCTGTAT	TTCACAGAGATATAAA	ACTGAAAAATATTCTA	399	
Db		302	GTGAACTTTTGTCA	CAAAACAACCTGCAT	CCATCGAGATGTAA	AGCCAGAAAAAGATCCTG	361	
Qy		400	ATAACTAAGCAAGAA	TAACTCAAGATTTGTG	ACTTCGGGTTGCAAAATTC	TCTGATT---	456	
Db		362	ATAACGAAGCACTCC	ATATCAAACTCTGTG	ACTTTCGGATTTGTCGCATGCTGACTGCG		421	
Qy		457	CCAGGAGATGCCAT	ACCGATTATGTAGCT	ACAGAGATGGTACCGAGCTCCTG	AACTTTCTT	516	
Db		422	CCAGGTGATTACTAC	ACAGACTACGTGGCA	ACAGGTGGTACCGCTCCC	CCAGAGCTGCTG	481	
Qy		517	GTGGGAGATCTCAG	TATGTTCTTCAGT	CGATATATGGGCTATTGGTTGTTGTTTTTGCA		576	
Db		482	GTGGGGACACGCA	GTATGGCCCTCCTGT	GGAACGTGTGGCAATAGAGCTGTGTTCTTGCG		541	
Qy		577	GAGCTCTGTGACGG	CCAGCCACTGTGG	CCCTGGAAAAATCAGATGTGG	ACCACCTTTATCTG	636	
Db		542	GAGCTGCTCTCGG	GGTGCCACTGTG	GCCCGGCNAAGTCACAGTGG	ACAGCTGTACCTC	601	
Qy		637	ATAATCAGAACACT	AGAAAAATTAAT	CCCCAAGACATCAAT	CTTTTAA--	AGGTAAAG	694
Db		602	ATCCGGAGAACAT	TGGGGATCTTAT	TCCAGGACCCAGCAAGTGGTT	TCAGACCAAAACC	661	

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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHES766113"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CS9CHN04"
/note="Organ: whole embryo; Vector: Site 1; EcorI; Site 2: NotI; T4 ligase; constructed from 1 million independent clones. Synthesis was initiated using methylated C in the first strand. Following this, first strand reaction was blunted, ligated to NotI and EcorI, size-selected, and cloned into compatible sites of a custom mpBlueScript (KS+) vector. The rounds using conditions adapted (1994) 91: 9228-9232 and Bonaldi (1996): 791, except that a single reannealing hybridization was

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```

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHES766113"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSEQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adaptors, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Ronaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

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QY 695 GGTTCCTCCAGTCAGTATACCTGAGCCAGAGACATCGAAACTCTTCAGGAAAG 753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
662 AGTTCTTCAGCGCGTACGATTCAGACCCAGAGCATGGGAGCCATTGGGCAATG 720

RESULT 9
CK482747 757 bp mRNA linear EST 14-JAN-2004
LOCUS AGENCOURT.17606510 NIH_MGC_235 Rattus norvegicus cDNA clone
DEFINITION IMAGE:7110321 5', mRNA sequence.
ACCESSION CK482747.1 GI:40827095
VERSION .
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapsb-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14977 Row: e Column: 07
High quality sequence stop: 695.
Location/Qualifiers
1. 757
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7110321"
/tissue_type="kidney, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_235"
/notes="Organ: kidney; Vector: pExpress-1; Site 1: EcorV;
Site 2: NotI; RNA obtained from pooled kidney tissue from
a mix of male and female animals at 8 wk old. Tissues were
snap-frozen before RNA extraction and purification
(tri-reagent method). cDNA was primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGGAGCGGCCCT(T)25-3' and
cloned into the EcorV/NotI sites of pExpress-1.
Size-selection >1.4kb resulted in an average insert size
of 2.2 kb. This primary library is non-normalized
(normalized primary library is NIH_MGC_236) and was
constructed by Express Genomics (Frederick, MD). Note:
this is a NIH_MGC library."

ORIGIN
Query Match 33.5%; Score 316.8; DB 7; Length 757;
Best Local Similarity 70.4%; Pred. No. 1.le-69;
Matches 439; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

QY 1 ATGGAAGATGATGAAATATGCTAGCTGGAAGAGGCTCTTATGGGTGTGATTCAAA 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
103 ATGGAAGATGCAAAAAATGGAAGATTGGAGAGGTTCTATGGGTAGTTTCAAG 162

QY 61 TGCAGAAACAAACCTCTGCAAGTAGTACTGTTTAAAAAATTTGGAATCTGAAGAT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
163 TGCAGAAACAGACACGCGGTTCAGATCGTGGCCATCAAGAGGTTCTTGGAAACCGAAGAT 222
QY 121 GATCTCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 223 GACCTGTCTATAAGAAAAATCGCCTTCGAGAAATCCGATGCTCAAGCAACTCAAGCAT 282
QY 181 CCAAAATCTGTGAACCTCATCGAGGTGTTTCAGAGAAAAAGGAAATGCAATTTAGTTTTT 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
283 CCCAACCTCGTCAGCCTCTCGGAAGTCTTCGCGAGGAAGCGGGCTTCACCTGGTGTTC 342
QY 241 GAATACCTGTGATCATACACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
343 GAGTACTGCCACACACACGCGTCTTCAGAGCTGGACAGATATCAGAGGGGGGTACAGAG 402
QY 301 GGAGTGATCAAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTCTATACAT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
403 CCTCTCGTGAAGAACATAAATCTGCGACACACTCGAGGCTGTGAATTTCTGCCATAAACAC 462
QY 361 AACTGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
463 AACTGCATACACAGAGATGTGAAGCCGGAACAATTTCTATCACCACCAACTCAGTCATT 522
QY 421 AAGATTGTGACTTCGGGTTTGCACAAAATTTCTGATT--CCAGGAGATGCTACACCGAT 477
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
523 AAGCTCTGTGACTTTGGTTTGCACGGCTTCTCAGCTGGACCTGGTACTACTACATGAC 582
QY 478 TATGTAGCTACGAGATGCTACCGAGCTCCCTGAATTTCTTGTGGGAGATATCTAGTATGGT 537
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
583 TACGTGCCACACAGGTGTACCGCTCACCTGAGCTGCTAGTGGGAGACACACAGTATGGC 642
QY 538 TCTTCAGTCGATATATGGGCTATTGGTTGTTTTCAGAGCTCTCTGACAGGCCAGCCA 597
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
643 CCCCCAGTAGATGCTGGGCAATTTGGGTGTGTTTGTGCTGAGTTGCTGTCGCGAGTGCCT 702
QY 598 CTGTGGCCTGGAAAAATCAGATGTG 621
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
703 CTGTGGCCAGGAAAAATCGATGTG 726

RESULT 10
AA061797 938 bp mRNA linear EST 03-FEB-1997
LOCUS ml34h09.r1 Stratagene mouse testis (#937308) Mus musculus cDNA
DEFINITION clone IMAGE:513953 5', similar to gb:U66358 SERINE/THREONINE-PROTEIN
KINASE KIALRE (HUMAN); mRNA sequence.
ACCESSION AA061797
VERSION AA061797.1 GI:1555606
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 938)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307801
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 442.
Location/Qualifiers
1. 938
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
FEATURES
source

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/db_xref="taxon:10090"
 /clones="IMAGE:513953"
 /sex="males"
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 /dev_stage="10-12 week old"
 /lab_host="SOUR (kanamycin resistant)"
 /clone_lib="Stratagene mouse testis (#937308)"
 /note="Organ: testis; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dr. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
 -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3' "

ORIGIN

Query Match 33.5%; Score 316.8; DB 1; Length 938;
 Best Local Similarity 82.9%; Pred. No. 1.1e-69;
 Matches 398; Conservative 0; Mismatches 77; Indels 5; Gaps 3;

Qy 135 GAAATAGCACTAGAGAAATACGTATGTTGAAGCAATTAAACATCCAAATCTGTGAA 194
 Db 1 GAAATAGCCCTGCGGAAATCCGTGCTGAAG---TTGAACACCCAAACCTCGTGA 57
 Qy 195 CCTCATCGAGTGTTCAGAGAAAGAAAGAAATGCAATTTAGTTTGAATCTGTGATCA 254
 Db 58 CCTCATCGAGTGTTCAGAGAAAGAAAGATGCAATTTAGTTTGAATCTGTGATCA 117
 Qy 255 TACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAG 314
 Db 118 CACACTGTAAACGAGCTGGAGAGAAACCCAAACGGAGTTCTGATGGAGTGATTAAG 177
 Qy 315 CGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACATACCTGATTCAG 374
 Db 178 TGTGCTATGGCAACCCCTTCAAGCCCTTAACCTTCTGTCAAGCACAAATTTGATTCATCG 237
 Qy 375 AGATATAAACCTGAAATATTTCTAATACTAAGCAAGGAATATCAAGATTTCTGACTT 434
 Db 238 GGATGTAAACCTGAAACATCTTAATAACCAAGCAAGGAGATGAAGATTTGTGACTT 297
 Qy 435 CGGTTTTCACAAATTTCTGATTCAGGAGATGCCCTACACCGCATTTATGTAGCTACGAGATG 494
 Db 298 TGGATTTGCAGAAATCTAATTCAGGAGAGCGCTACACAGACTATGTTGCCACCGATG 357
 Qy 495 GTACCGAGCTCTGAATCTTGTGGGAGATACCTCAGTATGTTCTTCAGTCGATATATG 554
 Db 358 GTACCGAGCCCGCAATCTCTGTTGGGAGACACGAAGTACGGTCTCTGTAGACGTGTG 417
 Qy 555 GGCTATTGTTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTGTGGCTGGAAATC 614
 Db 418 GGCCGTGCGTGTGTTTTCAGAG-CTCCTGACGGGTGAG-CACTCTGGCCGGGAAAC 475

RESULT 11

AV986182 598 bp mRNA linear EST 14-MAR-2002
 LOCUS AV986182 Nori Satoh unpublished cDNA library, larva Ciona
 DEFINITION intestinalis cDNA clone cilv41b18 5', mRNA sequence.
 VERSION AV986182
 KEYWORDS EST.

SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 phlebobranchia; Cionidae; Ciona.
 1 (bases 1 to 598)
 Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
 Expressed genes in Ciona intestinalis
 Unpublished (2000)
 JOURNAL Contact: Nori Satoh
 COMMENT Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source 1..598
 location/Qualifiers
 /organism="Ciona intestinalis"
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 /clones="cilv41b18"
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 /clone_lib="Nori Satoh unpublished cDNA library, larva"

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Query Match 32.5%; Score 306.8; DB 2; Length 598;

Best Local Similarity 70.7%; Pred. No. 3.7e-67;
 Matches 423; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

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 Qy 488 CGAGATGTTACCGAGCTCTGAACTTCTTGTGGAGATACACTAGTATGTTCTTCAGTCTG 547
 Db 481 CTAGGTGTACAGACACCTGAGCTCTCGTGGGGACACTCAGTATGGCCCTCCAGTGG 540
 Qy 548 ATATATCGGCTATTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCAGCTGTGGCC 605
 Db 541 ATGTGTGGCAATAGTTGCGTATTGCCGAGTTGTTGTGCGGACAGCATATTTGGCC 598

RESULT 12

CK472415

LOCUS CK472415

DEFINITION AGENCOURT 17613484 NIH MGC_236 Rattus norvegicus cDNA clone
 IMAGE:7127611 5', mRNA sequence.

VERSION CK472415

KEYWORDS CK472415.1 GI:40816513

SOURCE EST.

ORGANISM Rattus norvegicus (Norway rat)

REFERENCE Rattus norvegicus

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 806)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999).
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacob
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15022 row: e column: 17
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Location/Qualifiers
1. 806
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/note="Organ: kidney; Vector: pExpress-1; Site 1: EcorV;
Site 2: NotI; RNA obtained from pooled kidney tissue from
a mix of male and female animals at 8 wk old. Tissues were
snap-frozen and kept at -80C for two days before RNA
extraction and purification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTTGTCTAGATCGGCGGCCGC(T)25-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 2.2 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 235) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH MGC library."

ORIGIN

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212	GGAGAAAAGGAAAATGCAATTTAGTTTGTGAAATCTCTGTGATCATACACTTTTAAATGAGC	271		
61	GCAGGAAGCGCGGCTTCACCTGGTGTTCAGTACTGCCACCAACGGTGTCTTCAGGAGC	120		
272	TGGAAGAAACCCAAATGAGTTGCTTGATGGAGTGATCAAAAGCGTATTATGCGCAACAC	331		
121	TGGAAGATATCAGAGGGGGTACAGAGCCTCTCTGGAAGAACATAACTTGGCAGACAC	180		
332	TTCAAGCTCTTAATTTCTGTCTATPATACATAAATGTTATTCACAGAGATATAAAACCTGAAA	391		
181	TGCAGGCTGTGAATTTCTGCCTAAACACAACTGTCATACACAGAGATGTAAGACCCGAAA	240		
392	ATATTTCTAATAACTAGCAAGGAATAAATCAAGATTTTGTGACTTCGGGTTTGACAAATTC	451		
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452	TGATTT---CCAGAGATGCTTACCCGATATGTAGTACGAGATGGTACCGAGCTCTTG	508		
301	TCACATGGACCTGGTGACTACTACACTGACTACGTGGCCACCAAGTGGTACCGCTCACCTG	360		
509	AACTTTCTTGTGGAGATACCTCAGTATGGTTCTTTCAGTCGATATATCGGCTATTGGTTTG	568		
361	AGCTGCTAGTGGAGACACACAGTATGGCCCCCAGTAGATGCTGGGCATTTGGGTGTG	420		
569	TTTTTGCAGAGCTCTCTGACAGGCCAGCCACTGTGGCGCTGGAAAATCAGATGTGGACCAAC	628		
421	TGTTTTGCTGAGTTGCTGTCGAGAGTSCCTCTGTGGCCAGGAAAATCCGATGTGGACGAGC	480		

QY	629	TTTATCTGATTAATCAGAACACATAGGAAATTAATCCCAAGACATCAATCAATCTTTTAAAA	688
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QY	689	GTAACGGGTGTTTTCCATCGGCATCAGTATACCTTGAGCCAGAGACATGGAAACTCTTTGAGG	748
Db	541	TGATCAGTACTTCAGTGGGTGAAATTCAGACCCCTGAGACATCGAAGACACCTTGAGT	600
QY	749	AAAAGTTCTCAGATGTTCAATCCTGTGGCTCTGAACTTCATGAAGG	793
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BP016186			
LOCUS	BP016186	597 bp	mRNA linear EST 15-MAR-2001
DEFINITION	BP016186 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciad64e08 5', mRNA sequence.		
ACCESSION	BP016186		
VERSION	BP016186.1 GI:19507663		
KEYWORDS	EST.		
SOURCE	Ciona intestinalis		
ORGANISM	Ciona intestinalis		
REFERENCE	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.		
AUTHORS	1 (bases 1 to 597)		
TITLE	Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.		
JOURNAL	Expressed genes in Ciona intestinalis		
COMMENT	Unpublished (2000) Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp.		
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Qy	2	TGGAATAAGTATGAAAAATTAGCTAAGACTCGAGAGAGGCTCTTATGGGGTTGTATTTCAAAT	61		
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Qy	122	ATCCTGTGTGTTAAGAAATAGCACTAGAGAAATACGTATGTTGAAGCAATTTAAACATC	181		
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Qy	182	CAAAATCTGTGGAACCTCATCCGAGTGTTCCAGGAGAAAAAGGAAATGCATTTAGTTTTTG	241		
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Qy 302 GAGTGATCAAAAGCGTATTATGCGCAACACCTTCAGCTCTTAATTTCTGTCTATACATA 361
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Qy 362 ACTGTATTACAGAGATATAAAACCTGAAATATTCTAATAAATAAGCAAGCAATAATCA 421
Db 398 ATTGTATACATCGTGATGTAACCAAGAGACATATTAACTAAGCAAGGTGTATCA 457
Qy 422 AGATTGTGACTTCGGGTTTGACAAATCTTGA---TTCCAGGAGATCCCTACACCGAAT 478
Db 458 AGTTGTGTGACTTTGGATTTCAGAAATTTTAACTGGTCTCGCGCAGCATTAACCGACT 517
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RESULT 14
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LOCUS Rattus norvegicus LRRGT00026 mRNA, complete cds.
DEFINITION AY383681
ACCESSION AY383681.1 GI:37654267
VERSION AY383681.1
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1956)
Xu, C.S., Chang, C.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y.,
Yang, K.J., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Xing, X.K.,
Shen, G.M., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Liver regeneration after PH
Unpublished
2 (bases 1 to 1956)
Xu, C.S., Chang, C.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y.,
Yang, K.J., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Xing, X.K.,
Shen, G.M., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Direct Submision
Submitted (09-SEP-2003) Henan Bioengineering Key Lab, Henan Normal
University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China
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Qy 539 CTTCAGTCGATATATGGGC 557
Db 578 CTNCAGTGGATGTGGGC 596

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Matches 458; Conservative 0; Mismatches 282; Indels 3; Gaps 1;

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RESULT 15
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DEFINITION CB400506
ACCESSION CB400506
VERSION CB400506.1 GI:30742233
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.
1 (bases 1 to 565)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
```

Tolias,P.P., Ptacek,J., Snyder,M., Huang,M., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression

Nat. Genet. (2003) In press
Contact: Vidal M

Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739

Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david.hill@fci.harvard.edu or
marc.vidal@fci.harvard.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

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all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
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ORIGIN

Query Match	28.6%	Score 269.8	DB 6	Length 565
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 23:37:20 ; Search time 3580.63 Seconds
(without alignments)
1602.273 Million cell updates/sec

Title: US-10-766-691-11

Perfect score: 945

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	19	US-10-766-691-11
2	929	98.3	972	19	US-10-766-691-5
3	927	98.1	1790	17	US-10-333-314-30
4	868.8	91.9	1678	18	US-10-250-889-6
5	839	88.8	1041	19	US-10-766-691-9
6	823	87.1	1068	19	US-10-766-691-3
7	647	68.5	687	9	US-09-834-496A-3
8	647	68.5	882	9	US-09-834-496A-1
9	507	53.7	1819	19	US-10-766-691-13
10	454.4	48.1	561	19	US-10-766-691-1
11	454.4	48.1	594	19	US-10-766-691-7

Sequence 146, App
Sequence 1079, Ap
Sequence 24573, A
Sequence 5, Appli
Sequence 3, Appli
Sequence 107, Appl
Sequence 107, Appl
Sequence 33, Appl
Sequence 112, App
Sequence 114, App
Sequence 4494, Ap
Sequence 28, Appl
Sequence 137, App
Sequence 1037, Ap
Sequence 7854, Ap
Sequence 324, App
Sequence 30, Appl
Sequence 40, Appl
Sequence 84, Appl
Sequence 718, App
Sequence 1165, Ap
Sequence 985, App
Sequence 40, Appl
Sequence 7, Appli
Sequence 668, App
Sequence 4, Appli
Sequence 668, App
Sequence 3111, Ap
Sequence 2447, Ap
Sequence 3111, Ap
Sequence 3745, Ap
Sequence 4192, Ap
Sequence 7455, Ap
Sequence 420, App
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-766-691-11
; Sequence 11, Application US/107666691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 945
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-11

Query Match 100.0%; Score 945; DB 19; Length 945;
Best Local Similarity 100.0%; Pred. No. 2.8e-238;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGGAAGATGATAAAATTAGCTAGACGGAGCGGCTTATGGGTGTATTCAAA 60
|||||

Db 1 ATGGAAGATGATAAATAGCTAAGACTGGAGAGGCTTATGGGTTGTATTCAA 60
Qy 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTCTTAAATAATTTGCGAATCTGAGAT 120
Db 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTCTTAAATAATTTGCGAATCTGAGAT 120
Qy 121 GATCCTCTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGGAAGCAATTAACACAT 180
Db 121 GATCCTCTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGGAAGCAATTAACACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAGAAATGCAATTTAGTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAGAAATGCAATTTAGTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Qy 421 AAGATTGTGACTTCGGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 480
Qy 481 GTAGCTACGAGATGCTTACCGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 540
Db 481 GTAGCTACGAGATGCTTACCGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 540
Qy 541 TCAGTCGATATATGGGCTATTTGTTGTTTTCAGAGCTCTTCAAGCTCTTAAATTTCTGTCTATATACAT 600
Db 541 TCAGTCGATATATGGGCTATTTGTTGTTTTCAGAGCTCTTCAAGCTCTTAAATTTCTGTCTATATACAT 600
Qy 601 TGGCCTGGAAATCAGATGTTGAGCAACTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 660
Db 601 TGGCCTGGAAATCAGATGTTGAGCAACTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 660
Qy 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 720
Db 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 720
Qy 721 GAGCCAGAGACATGGAACCTTTGAGAAAGTTCTCAGATGTTCACTCTGTGGCTCTG 780
Db 721 GAGCCAGAGACATGGAACCTTTGAGAAAGTTCTCAGATGTTCACTCTGTGGCTCTG 780
Qy 781 AACTTCATGAAGGGTCTCTGAGATGAATCCAGATGACAGATTAACCTGTTCCCACTC 840
Db 781 AACTTCATGAAGGGTCTCTGAGATGAATCCAGATGACAGATTAACCTGTTCCCACTC 840
Qy 841 CTGAGAGCTCTCTACTTGTATTCTTTTAAAGGCGCCAAATTAAGAAAGACAGTAAAT 900
Db 841 CTGAGAGCTCTCTACTTGTATTCTTTTAAAGGCGCCAAATTAAGAAAGACAGTAAAT 900
Qy 901 GAAGGAAGAAACAGAGACCGCAACAGGTACTTCCGCTCAAAAGT 945
Db 901 GAAGGAAGAAACAGAGACCGCAACAGGTACTTCCGCTCAAAAGT 945

RESULT 2

US-10-766-691-5
; Sequence 5, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2004-01-28
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 972
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-691-5

Query Match 98.3%; Score 929; DB 19; Length 972;
Best Local Similarity 100.0%; Pred. No. 4,7e-234; Indels 0; Gaps 0;
Matches 929; Conservative 0; Mismatches 0;

Qy 1 ATGGAAGATGATAAATAGCTAAGACTGGAGAGGCTTATGGGTTGTATTCAA 60
Db 1 ATGGAAGATGATAAATAGCTAAGACTGGAGAGGCTTATGGGTTGTATTCAA 60
Qy 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTTAAATAATTTGCGAATCTGAGAT 120
Db 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTTAAATAATTTGCGAATCTGAGAT 120
Qy 121 GATCCTCTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGGAAGCAATTAACACAT 180
Db 121 GATCCTCTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGGAAGCAATTAACACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAGAAATGCAATTTAGTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAGAAATGCAATTTAGTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Qy 421 AAGATTGTGACTTCGGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 480
Qy 481 GTAGCTACGAGATGCTTACCGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 540
Db 481 GTAGCTACGAGATGCTTACCGGTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATTAT 540
Qy 541 TCAGTCGATATATGGGCTATTTGTTGTTTTCAGAGCTCTTCAAGCTCTTAAATTTCTGTCTATATACAT 600
Db 541 TCAGTCGATATATGGGCTATTTGTTGTTTTCAGAGCTCTTCAAGCTCTTAAATTTCTGTCTATATACAT 600
Qy 601 TGGCCTGGAAATCAGATGTTGAGCAACTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 660
Db 601 TGGCCTGGAAATCAGATGTTGAGCAACTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 660
Qy 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 720
Db 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAAACCGGTTTTCATGGCATCAGTATACCT 720
Qy 721 GAGCCAGAGACATGGAACCTTTGAGAAAGTTCTCAGATGTTCACTCTGTGGCTCTG 780
Db 721 GAGCCAGAGACATGGAACCTTTGAGAAAGTTCTCAGATGTTCACTCTGTGGCTCTG 780

QY 781 AACTTCATGAGGGGTCTGAGATGAATCCAGATGACAGTAACTTACCTGTTCCTCAACTC 840
DB 781 AACTTCATGAGGGGTCTGAGATGAATCCAGATGACAGTAACTTACCTGTTCCTCAACTC 840
QY 841 CTGAGAGCTCTACTCTTTGATCTTTTCAAGAGGGCCCAAAATTTAAAGAAAAGCAGTAAT 900
DB 841 CTGAGAGCTCTACTCTTTGATCTTTTCAAGAGGGCCCAAAATTTAAAGAAAAGCAGTAAT 900
QY 901 GAAGGAAGAAACAGAAAGCGCCCAACAGGT 929
DB 901 GAAGGAAGAAACAGAAAGCGCCCAACAGGT 929

RESULT 3

US-10-333-314-30
; Sequence 30, Application US/10333314
; Publication No. US20030211093A1

GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Danielle B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIZTEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.

; TITLE OF INVENTION: HUMAN KINASES

; FILE REFERENCE: PI-0162 USN

; CURRENT APPLICATION NUMBER: US/10/333,314

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: PCT/US01/23092

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/220,038

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/222,112

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,831

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/224,729

; PRIOR FILING DATE: 2000-08-11

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PERL Program

; SEQ ID NO 30

; LENGTH: 1790

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 1698381CB1

US-10-333-314-30

Query Match

Best Local Similarity 98.1%; Score 927; DB 17; Length 1790;

Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAGATGAAATTAAGCTAAGCTGAGAGGGTCTTATGGGTGTGTAATCAAA 60
DB 239 ATGAAAGATGAAATTAAGCTAAGCTGAGAGGGTCTTATGGGTGTGTAATCAAA 298
QY 61 TGCAGAAACAAACCTCTGGAACAAGTAGTACTGTAAAAAATTTGTGGAATCTGAAGAT 120
DB 299 TGCAGAAACAAACCTCTGGAACAAGTAGTACTGTAAAAAATTTGTGGAATCTGAAGAT 358
QY 121 GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180

DB 359 GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 418
QY 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGGAAAAAGGAAATGATCATTTAGTTTTT 240
DB 419 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGGAAAAAGGAAATGATCATTTAGTTTTT 478
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAAACCCAAATGGAGTGTCTGAT 300
DB 479 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAAACCCAAATGGAGTGTCTGAT 538
QY 301 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAAATTTCTGTGCATATACAT 360
DB 539 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAAATTTCTGTGCATATACAT 598
QY 361 AACTGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
DB 599 AACTGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 658
QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCGTATTCAGGAGATGCTTACACCGATTAT 480
DB 659 AAGATTTGTGACTTCGGGTTTGCACAAATTCGTATTCAGGAGATGCTTACACCGATTAT 718
QY 481 GTACCTACGAGATGTCACCGAGCTCCTGAACTCTTGTGGGAGATACTCAGTATGTTCT 540
DB 719 GTACCTACGAGATGTCACCGAGCTCCTGAACTCTTGTGGGAGATACTCAGTATGTTCT 778
QY 541 TCAGTGCATATATGGGCTATTGGTGTGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 600
DB 779 TCAGTGCATATATGGGCTATTGGTGTGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 838
QY 601 TGGCTCGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAACACTAGGAAAAATTA 660
DB 839 TGGCTCGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAACACTAGGAAAAATTA 898
QY 661 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTTCCATGGCATCATGATACCT 720
DB 899 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTTCCATGGCATCATGATACCT 958
QY 721 GAGCCAGAGACATGGAACCTTTTGAGGAAAAAGTTCTCAGATGTTTCATCTGTGGCTGTG 780
DB 959 GAGCCAGAGACATGGAACCTTTTGAGGAAAAAGTTCTCAGATGTTTCATCTGTGGCTGTG 1018
QY 781 AACTTCATGAAGGGGTGCTGGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAACTC 840
DB 1019 AACTTCATGAAGGGGTGCTGGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAACTC 1078
QY 841 CTGAGAGCTCTACTTTTGTGATCTTTTCAAGAGGCCCAAAATTTAAAGAAAAGCAGTAAT 900
DB 1079 CTGAGAGCTCTACTTTTGTGATCTTTTCAAGAGGCCCAAAATTTAAAGAAAAGCAGTAAT 1138
QY 901 GAAGGAAGAAACAGAAAGCGCCCAACAG 927
DB 1139 GAAGGAAGAAACAGAAAGCGCCCAACAG 1165

RESULT 4

US-10-250-889-6

; Sequence 6, Application US/10250889

; Publication No. US20040115629A1

; GENERAL INFORMATION:

; APPLICANT: PANZER, Scott R.; LINCOLN, Stephen E.;

; APPLICANT: ALTUS, Christina M.; DUFOUR, Gerard E.;

; APPLICANT: JACKSON, Jennifer L.; JONES, Anissa L.;

; APPLICANT: DAM, Tam C.; LIU, Tommy F.;

; APPLICANT: HARRIS, Bernard; FLORES, Vincent Z.;

; APPLICANT: DENO, Abel; MARWAHA, Akesh;

; APPLICANT: CHEN, Alice J.; CHANG, Simon C.;

; APPLICANT: GERSTIN, Jr., Edward H.; PERALTA, Careyna H.;

; APPLICANT: DAVID, Marie H.; LEWIS, Samantha A.

; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: PT-1195 USN

; CURRENT APPLICATION NUMBER: US/10/250,889

```

; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: PCT/US02/01009
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,864
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/262,207
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,164
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,215
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,102
; PRIOR FILING DATE: 2001-01-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No: LI:058298.1:2001JAN12
US-10-250-889-6

Query Match      91.9%; Score 868.8; DB 18; Length 1678;
Best Local Similarity 99.2%; Pred. No. 4.5e-218;
Matches 925; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

QY      1  ATGGAAGAGTATGAAAATTAGCTTAAGCTGGAAGGGCTTTATGGGTTGTAATCAAA 60
DB      131  ATGGAAGAGTATGAAAATTAGCTTAAGCTGGAAGGGCTTTATGGGTTGTAATCAAA 190

QY      61  TGCAGA-AACAAAACCTCTGACAAAGTAGTAGCTGTTAAAAAAATTTCTGGAATCTGAAGA 119
DB      191  TGCAGATAACAAAACCTCTGACAAAGTAGTAGCTGTTAAAAAAATTTCTGGAATCTGAAGA 250

QY      120  TGATCCTGTTGTTAAGAAATAGCACTAAGAAATACGTA-TGTTGAAGCAATTAAGAAC 178
DB      251  TGATCCTGTTGTTAAGAAATAGCACTAAGAAATACGTAAGAAATACGTAAGCAATTAAGAAC 310

QY      179  ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAAGCAAAATCGATTAGTTT 238
DB      311  ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAAGCAAAATCGATTAGTTT 370

QY      239  TTGAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAACCCAAATGGAGTTGCTG 298
DB      371  TTGAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAACCCAAATGGAGTTGCTG 430

QY      299  ATGGAGTGATCAAAAGGCTATTATGCAACACTTCAAGCTCTTAATTTCTGTCATATAC 358
DB      431  ATGGAGTGATCAAAAGGCTATTATGCAACACTTCAAGCTCTTAATTTCTGTCATATAC 490

QY      359  ATAACTGTATTCACAGATATATAAACCTGAAAATATTCTAATACTAAGCAAGGAATAA 418
DB      491  ATAACTGTATTCACAGATATATAAACCTGAAAATATTCTAATACTAAGCAAGGAATAA 550

QY      419  TCAAGATTTGTGACTCGGGTTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATT 478
DB      551  TCAAGATTTGTGACTCGGGTTTGCAAAATTTCTGATTCAGAGATGCTTACCGGATT 610

QY      479  ATGTAGCTA-CGAGATGGTACCGAGCT-CCTGAACCTTCTTGTGGGAGATACCT-CAGTATG 535
DB      611  ATGTAGCTAGCGAGATGGTACCGAGCTCCTGNACTTCTTGTGGGAGATACCTCAGTATG 670

QY      536  GTTCTTCAGTCAATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCTCTGACAGCCAGC 595
DB      671  GTTCTTCAGTCAATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCTCTGACAGCCAGC 730

QY      596  CACTGTGGCCCTGGAAATATCAGATGTGACCAACTTTATCTGATTAATCAGAACTAGGAA 655
DB      731  CACTGTGGCCCTTGAAATATCAGATGTGACCAACTTTATCTGATTAATCAGAACTAGGAA 790

QY      656  AATTAATCCCAAGACATCAATCAATCTTTAAAGCTTAACGGGTTTTTCCATGGCATGAGTA 715
DB      791  AATTAATCCCAAGACATCAATCAATCTTTAAAGCTTAACGGGTTTTTCCATGGCATGAGTA 850

QY      716  TACCTGAGCCAGAGACATGGAACACTCTTGAGGAAAAGTTCTCAGATGTTTCATCTGTGG 775
DB      851  TACCTGAGCCAGAGACATGGAACACTCTTGAGGAAAAGTTCTCAGATGTTTCATCTGTGG 910

QY      776  CTCTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTCCC 835
DB      911  CTCTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTCCC 970

QY      836  AACTCTGAGAGCTCTCTACTTTGATTTCTTTCAAGAGGCCCAAAATTAAGAAAAAGCAC 895
DB      971  AACTCTGAGAGCTCTCTACTTTGATTTCTTTCAAGAGGCCCAAAATTAAGAAAAAGCAC 1030

QY      896  GTAATGAAGGAAGAAACAGACAGACGCAACAG 927
DB      1031  GTAATGAAGGAAGAAACAGACAGACGCAACAG 1062

RESULT 5
US-10-766-691-9
; Sequence 9, Application US/10766691
; Publication No: US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-9

Query Match      88.8%; Score 839; DB 19; Length 1041;
Best Local Similarity 90.8%; Pred. No. 2.5e-210;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY      1  ATGGAAGATGAAAATTAAGCTTAAGCTGGAAGGGTCTTATGGGGTTGTAATCAAA 60
DB      1  ATGGAAGATGAAAATTAAGCTTAAGCTGGAAGGGTCTTATGGGGTTGTAATCAAA 60

QY      61  TGCAGAAAACAAACCTCTGGACAAAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 120
DB      61  TGCAGAAAACAAACCTCTGGACAAAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 120

QY      121  GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
DB      121  GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180

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QY 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAGGAAATGCATTAGTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAGGAAATGCATTAGTTT 240
QY 241 GAATACGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 241 GAATACGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
QY 361 AACTGTATTACAGAGATATAAAACCTTGAATAATTTCTAATACTAGCAAGGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTTGAATAATTTCTAATACTAGCAAGGAAATATC 420
QY 421 AAGATTGTGACTTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTTACACCGATTAT 480
Db 421 AAGATTGTGACTTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTTACACCGATTAT 480
QY 481 GTAGTACGAGATGGTACCGAGTCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGTCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
QY 541 TCAGTCGATATATGGGCTATTGTTGTTTTCAGAGATGCTTACACCGCAGCACTG 600
Db 541 TCAGTCGATATATGGGCTATTGTTGTTTTCAGAGATGCTTACACCGCAGCACTG 600
QY 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACACT- 650
Db 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACACTAGTAGAGACG 660
QY 651 ----- 650
Db 651 GGGTTTCGCCATGTTGACAGGCTGTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
QY 651 -----AGGAAATTAATCCAGACATCAATCAATCTTT 684
Db 721 GTAGCTCTCAAAAGTGTGGAAATACAGGAAATTAATCCAGACATCAATCAATCTTT 780
QY 685 AAAAGTAAACGGGTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 744
Db 781 AAAAGTAAACGGGTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 840
QY 745 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTGCTGAACTTCAATGAAGGGGTGCTGAAG 804
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTGCTGAACTTCAATGAAGGGGTGCTGAAG 900
QY 805 ATGAATCCAGATGACAGATTAACTGTTCCCACTCTCTGAGAGCTCTTACTTTGATCT 864
Db 901 ATGAATCCAGATGACAGATTAACTGTTCCCACTCTCTGAGAGCTCTTACTTTGATCT 960
QY 865 TTTTCAGAGGCCCAATTAAGGAAAGCAGCTAATGAAGGAAAGACAGAGACGCA 924
Db 961 TTTTCAGAGGCCCAATTAAGGAAAGCAGCTAATGAAGGAAAGACAGAGACGCA 1020
QY 925 CAGGTACTTCCGCTCAAAAGT 945
Db 1021 CAGGTACTTCCGCTCAAAAGT 1041

```

RESULT 6

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US-10-766-691-3
; Sequence 3, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and

```

```

; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-691-3

```

```

Query Match      87.1%; Score 823; DB 19; Length 1068;
Best Local Similarity 90.6%; Pred. No. 4.2e-206;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

```

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QY 1 ATGGAAGAATGATGAAAAATTTAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
Db 1 ATGGAAGAATGATGAAAAATTTAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
QY 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCTCTGTTCTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db 121 GATCTCTGTTCTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
QY 181 CCAAACTCTTGTGAACCTCATCGAGGTGTTCCAGGAGAAAAAGGAAAAATGCAATTTAGTTT 240
Db 181 CCAAACTCTTGTGAACCTCATCGAGGTGTTCCAGGAGAAAAAGGAAAAATGCAATTTAGTTT 240
QY 241 GAATACGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 241 GAATACGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGSCAAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGSCAAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAAATATC 420
QY 421 AAGATTGTGACTTTCGGGTTTGCAAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
Db 421 AAGATTGTGACTTTCGGGTTTGCAAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
QY 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGTTCT 540
QY 541 TCAGTCGATATATGGGCTATTGTTGTTTTCAGAGATGCTTCTGAGAGGCAAGCACT- 600
Db 541 TCAGTCGATATATGGGCTATTGTTGTTTTCAGAGATGCTTCTGAGAGGCAAGCACTG 600
QY 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACACTAGTAGAGACG 660
Db 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACACTAGTAGAGACG 660
QY 651 ----- 650
Db 651 GGGTTTCGCCATGTTGACAGGCTGTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
QY 651 -----AGGAAATTAATCCAGACATCAATCAATCTTT 684
Db 721 GTAGCTCTCAAAAGTGTGGAAATTAAGGAAATTAATCCAGACATCAATCAATCTTT 780
QY 685 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 744

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Db 781 AAAAGTAAACGGTCTTTTCCATGCAATCAGTATACCTAGCCAGAAACATGGAAATCTTT 840
QY 745 GAGGAAAAGTTTCAGATGTTTCCATGCTGCTCTGAATTCATGAAGGGGTCTCTGAAG 804
Db 841 GAGGAAAAGTTTCAGATGTTTCCATGCTGCTCTGAATTCATGAAGGGGTCTCTGAAG 900
QY 805 ATGAATCCAGATGACAGATTAACTCTGCCAATCTCTGAGAGCTCTCTAATTTGATTTCT 864
Db 901 ATGAATCCAGATGACAGATTAACTCTGCCAATCTCTGAGAGCTCTCTAATTTGATTTCT 960
QY 865 TTTCAAGAGGCCCAATTTAAAGAAAGACGCTTAATGAAGGAAGAAACAGAGAGCCCAA 924
Db 961 TTTCAAGAGGCCCAATTTAAAGAAAGACGCTTAATGAAGGAAGAAACAGAGAGCCCAA 1020
QY 925 CAGGT 929
Db 1021 CAGGT 1025

```

```

RESULT 7
US-09-834-496A-3
; Sequence 3, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-496A-3

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```

Query Match 68.5%; Score 647; DB 9; Length 687;
Best Local Similarity 99.2%; Pred. No. 7.8e-160;
Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGAGGGTCTTATGGGGTTGATTCAAA 60
Db 1 ATGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGAGGGTCTTATGGGGTTGATTCAAA 60
QY 61 TGCAGAAACAAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAAATAGCAATAGCTATGTTGAAGCAATTTAAACAT 180
Db 121 GATCCTATTTGTTAAGAAAATAGCAATAGCTATGTTGAAGCAATTTAAACAT 180
QY 181 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
QY 241 GAATACCTGTCATCATACACTTTTAAATGAGCTGGAAGAAACCCCAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTCATCATGACCTTTTAAATGAGCTGGAAGAAACCCCAATGGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTTATGGCAACAATTTCAAGCTCTTAAATTTCTGTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTTATGGCAACAATTTCAAGCTCTTAAATTTCTGTATATACAT 360
QY 361 AACTGTATTTACAGAGATATTAACCTGAAAATTTCTAATACTAAGCAAGGAATATTC 420
Db 361 AACTGTATTTACAGAGATATTAACCTGAAAATTTCTAATACTAAGCAAGGAATATTC 420

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QY 421 AAGATTTCGACTTCGGGTTTGCAAAATTCGATTCAGGAGATGCCTACACGATTTAT 480
Db 421 AAGATTTCGACTTCGGGTTTGCAAAATTCGATTCAGGAGATGCCTACACGATTTAT 480
QY 481 GTAGCTACGAGATGATACCGAGCTCCCTGAACCTCTTGTGGGAGATACCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGATACCGAGCTCCCTGAACCTCTTGTGGGAGATACCTCAGTATGGTTCT 540
QY 541 TCAGTTCGATATATGGGCTATTTGGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Db 541 TCAGTTCGATATATGGGCTATTTGGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
QY 601 TGGCTCGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGGAA 655
Db 601 TGGCTCGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGGTA 655

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RESULT 8
US-09-834-496A-1
; Sequence 1, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (129)...(815)
US-09-834-496A-1

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Query Match 68.5%; Score 647; DB 9; Length 882;
Best Local Similarity 99.2%; Pred. No. 8.8e-160;
Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGAGGGTCTTATGGGGTTGATTCAAA 60
Db 129 ATGGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGAGGGTCTTATGGGGTTGATTCAAA 188
QY 61 TGCAGAAACAAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 120
Db 189 TGCAGAAACAAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 248
QY 121 GATCCTGTTGTTAAGAAAATAGCAATAGCTATGTTGAAGCAATTTAAACAT 180
Db 249 GATCCTATTTGTTAAGAAAATAGCAATAGCTATGTTGAAGCAATTTAAACAT 308
QY 181 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 309 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 368
QY 241 GAATACCTGTCATCATACACTTTTAAATGAGCTGGAAGAAACCCCAATGGAGTTGCTGAT 300
Db 369 GAATACCTGTCATCATGCACTTTTAAATGAGCTGGAAGAAACCCCAATGGAGTTGCTGAT 428
QY 301 GGAGTGATCAAAAGCGTATTTATGGCAACAATTTCAAGCTCTTAAATTTCTGTATATACAT 360
Db 429 GGAGTGATCAAAAGCGTATTTATGGCAACAATTTCAAGCTCTTAAATTTCTGTATATACAT 488
QY 361 AACTGTATTTACAGAGATATTAACCTGAAAATTTCTAATACTAAGCAAGGAATATTC 420
Db 489 AACTGTATTTACAGAGATATTAACCTGAAAATTTCTAATACTAAGCAAGGAATATTC 548

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Qy 421 AAGATTGTGACTTCGGGTTGGCAAAATCTGATTCAGAGAGATGCTACACCGATTAT 480
 Db 549 AAGATTGTGACTTCGGGTTGGCAAAATCTGATTCAGAGAGATGCTACACCGATTAT 608
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACCTCTGTGGGAGATACCTCAGTATGGTTCT 540
 Db 609 GTAGCTACGAGATGGTACCGAGCTCCTGAACCTCTGTGGGAGATACCTCAGTATGGTTCT 668
 Qy 541 TCAGTCGATATATGGGCTATTGGTGTGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 600
 Db 669 TCAGTCGATATATGGGCTATTGGTGTGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 728
 Qy 601 TGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATATCAAGAACACTAGGAA 655
 Db 729 TGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATATCAAGAACACTAGGTA 783

RESULT 9

US-10-766-691-13
 ; Sequence 13, Application US/10766691
 ; Publication No. US20050042626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/10766,691
 ; PRIOR FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 1819
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-766-691-13

Query Match 53.7%; Score 507; DB 19; Length 1819;
 Best Local Similarity 69.8%; Pred. No. 9.8e-123;
 Matches 929; Conservative 0; Mismatches 0; Indels 402; Gaps 2;
 Qy 1 ATGGAAGAATGAAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGTTGTATTCAA 60
 Db 138 ATGGAAGAATGAAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGTTGTATTCAA 197
 Qy 61 TGCAGAAACAAACCTCTGGAAGATAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
 Db 198 TGCAGAAACAAACCTCTGGAAGATAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 257
 Qy 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db 258 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 317
 Qy 181 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGAGAAAAAGAAAAATGCAATTTAGTTT 240
 Db 318 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGAGAAAAAGAAAAATGCAATTTAGTTT 377
 Qy 241 GAATATCTGTATCATACATCTTTTAAATAGAGTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
 Db 378 GAATATCTGTATCATACATCTTTTAAATAGAGTGGAAAGAAACCCAAATGGAGTTGCTGAT 437
 Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
 Db 438 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 497

Qy 361 AACTGTATTACAGAGATATAAAACCTGAAAAATATTCTTAATACTAAGCAAGGAATATC 420
 Db 498 AACTGTATTACAGAGATATAAAACCTGAAAAATATTCTTAATACTAAGCAAGGAATATC 557
 Qy 421 AAGATTGTGACTTCGGGTTTGCACAAATCTG----- 453
 Db 558 AAGATTGTGACTTCGGGTTTGCACAAATCTGAGTTGGACTTCATCTTCTCTGGTGCC 617
 Qy 454 ----- 453
 Db 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAAATCTTTTTCTGCCAATTCAGAGATTTT 677
 Qy 454 ----- 453
 Db 678 CTCCTGGCTTTGGATCCATTGCTGACACAGTGTTTTCAACATGGGGCCCGGCTCATCTCGA 737
 Qy 454 ----- 453
 Db 738 ACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCCTCCCAAAGTCTGGATTGCAAGTGTG 797
 Qy 454 ----- 453
 Db 798 AGCCACCGTCCCGACCCAGATTTTCAAACAATAACTACTGAGAGCTCACAAGATTGTTT 857
 Qy 454 -----ATTCCAGAGATGCCCTACACC 474
 Db 858 TTATGTGGGAACACAAATTTTCGAACAAATTTCTTGGAACGCATTCAGGAGATGCCCTACACC 917
 Qy 475 GATTATGTAGCTACGAGATGTCACGAGCTCCTGAACCTCTTGTGGGAGATPACTCAGTAT 534
 Db 918 GATTATGTAGCTACGAGATGTCACGAGCTCCTGAACCTCTTGTGGGAGATPACTCAGTAT 977
 Qy 535 GGTTCCTTCAGTCGATATATGGGCTATTGGTGTGTTTTTTCAGAGCTCCTGACAGGCCAG 594
 Db 978 GGTTCCTTCAGTCGATATATGGGCTATTGGTGTGTTTTTTCAGAGCTCCTGACAGGCCAG 1037
 Qy 595 CCAGTGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATTAATCAGAACACT----- 650
 Db 1038 CCAGTGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATTAATCAGAACACTAGTA 1097
 Qy 651 ----- 650
 Db 1098 GAGACGGGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTTCGAGCTCAAGTGATCCA 1157
 Qy 651 -----AGGAAAAATTAATCCCAAGACATCAATCA 678
 Db 1158 CCTGCCGTAGCTCTCAAGAGTGTGGAATTTACAGGAAAAATTAATCCCAAGACATCAATCA 1217
 Qy 679 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 738
 Db 1218 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 1277
 Qy 739 ACTCTTCAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGGTGT 798
 Db 1278 ACTCTTCAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGGTGT 1337
 Qy 799 CTGAAGATGAATCCAGATGACAGATTAACTGTTTCCCAACTCTCTGGAGAGCTCCTACTTTT 858
 Db 1338 CTGAAGATGAATCCAGATGACAGATTAACTGTTTCCCAACTCTCTGGAGAGCTCCTACTTTT 1397
 Qy 859 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCAGTAAATGAAGAGAAACAGAGAAGA 918
 Db 1398 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCAGTAAATGAAGAGAAACAGAGAAGA 1457
 Qy 919 CGCCAACAGGT 929
 Db 1458 CGCCAACAGGT 1468

RESULT 10
 US-10-766-691-1
 ; Sequence 1, Application US/10766691
 ; Publication No. US20050042626A1

```

; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-1

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Query Match      48.1%; Score 454.4; DB 19; Length 561;
Best Local Similarity 99.8%; Pred. No. 3.9e-109;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAAGATGATGAAATTTAGCTAAGACTGAGAGAGGCTCTTATGGGTTGTATTCAAA 60
DB 1 ATGGAAGATGATGAAATTTAGCTAAGACTGAGAGAGGCTCTTATGGGTTGTATTCAAA 60
QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
DB 61 TGCAGAAACAAACCTCTGGCAAGTAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTTAAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 180
DB 121 GATCCTGTTGTTTAAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 180
QY 181 CCAATCTGTGTAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
DB 181 CCAATCTGTGTAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
DB 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
DB 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
QY 361 AACTGTATTCACAGATATATAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
DB 361 AACTGTATTCACAGATATATAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456
DB 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456

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RESULT 11
US-10-766-691-7
; Sequence 7, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and

```

```

; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-7

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```

Query Match      48.1%; Score 454.4; DB 19; Length 594;
Best Local Similarity 99.8%; Pred. No. 4e-109;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAAGATGATGAAATTTAGCTAAGACTGAGAGAGGCTCTTATGGGTTGTATTCAAA 60
DB 1 ATGGAAGATGATGAAATTTAGCTAAGACTGAGAGAGGCTCTTATGGGTTGTATTCAAA 60
QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
DB 61 TGCAGAAACAAACCTCTGGCAAGTAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTTAAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 180
DB 121 GATCCTGTTGTTTAAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 180
QY 181 CCAATCTGTGTAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
DB 181 CCAATCTGTGTAAGAAATAGCAGTAAGAGTAAGTGTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
DB 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
DB 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
QY 361 AACTGTATTCACAGATATATAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
DB 361 AACTGTATTCACAGATATATAACCTGAAATATTCTTAATACTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456
DB 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456

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RESULT 12
US-10-363-616-146
; Sequence 146, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 146
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (463)..(1539)

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US-10-363-616-146

Query Match 44.0%; Score 415.4; DB 17; Length 1612;
Best Local Similarity 66.7%; Pred. No. 1.3e-98;
Matches 609; Conservative 0; Mismatches 301; Indels 3; Gaps 1;
Qy 1 ATGGAAAGTATGAAAATTAAGCTTAAGCTGAGAGGGTCTTATGGGTGTATTTCAA 60
Db 466 ATGGAGAAGTATGAAAATTAAGCTTAAGCTGAGAGGGTCTTATGGGTGTATTTCAA 525
Qy 61 TGCAGAAACAAACCTCTGGACAAAGTAGTACTGTGTTAAAAATTTGGGAATCTGAAGAT 120
Db 526 TGTAGAAACAGGACACGGGTGAGTTGTGCCATCAAGAAGTTCTGGAATCAGAAGAT 585
Qy 121 GATCCTGTGTTAAGAAATAAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db 586 GACCCCTGTATAGAAATAAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 645
Qy 181 CCAATCTGTGAACCTCATCGAGGTGTTACAGGAGAAAGAAATGCAATTTAGTTT 240
Db 646 CCCAACCTTGTAACTCTCGGAAGTCTTACAGGAGAAACGGAGGCTTCACCTGGTGT 705
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAAGTTGCTGAT 300
Db 706 GAATATTTGACACACACAGTTCTCCATGAGTTGGACAGATACCAAGGGGTACACGAA 765
Qy 301 GGAGTGATCAAAAGCGTATTATGGAACAACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 766 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAATTTTGGCATAAACAC 825
Qy 361 AACTGTATTACAGAGATATAAAACCTTGAATTAATTTCTAATACATAGCAAGGAATATC 420
Db 826 AATTGCAATACATAGAGACGTGAAGCCAGAAATATCTCTCATACAGAAACATTTCCGTGAT 885
Qy 421 AAGATTGTGACTTTCGGTTTGCACAAATCTCGATT---CCAGAGAGATGCTACACCGAT 477
Db 886 AAGCTTTGTGACTTTGGAATTTGCTCGGCTTTTGAAGCCAGTACTACTATACAGAC 945
Qy 478 TATGTAGCTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATACCTCAGTATGGT 537
Db 946 TACGTGCTACCGAGTGTACCGCTCCCTGAGCTGCTGTGGGGGACACGCGTACGGC 1005
Qy 538 TCTTCAGTCGATATATGGGCTATTTGGTTGTGTTTGGAGAGCTCTGACAGGGCAGCCA 597
Db 1006 CCCCCTGGTATGTTTGGGCAATTTGGCTGTCTTGTGAGCTGCTGTACAGAGTGCCT 1065
Qy 598 CTGTGGCTTGAAATCAGATGTGCAACCACTTTATCTGATAATCAGAACACTAGGAAA 657
Db 1066 CTGTGGCCAGGAAATCGAGTGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGAT 1125
Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATA 717
Db 1126 CTCATCTAGCCACAGCAAGTGTATTAGCAAGAAATCAGTACTTTCAGTGGAGTGAAT 1185
Qy 718 CTTGAGCCAGAGACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTCACTGTGGCT 777
Db 1186 CCAGACCTTGAAGATATGGAACCACTTTGAATTTAAATTTCCCAACATCTCTTATCTGCC 1245
Qy 778 CTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAA 837
Db 1246 CTGGGGCTCTTAAGGGGTGCTCCACATGAGCCCTACTGAAGGCTGACATGTGAACAG 1305
Qy 838 CTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAATTTAAAGAAAGACGAT 897
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Qy 898 AATGAAGAAGAA 910
Db 1366 AACAAACCAACAA 1378

RESULT 13

US-09-960-706-1079

; Sequence 1079, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1079
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66358
US-09-960-706-1079

Query Match 43.8%; Score 413.8; DB 10; Length 1363;
Best Local Similarity 66.6%; Pred. No. 3e-98;
Matches 608; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

Qy 1 ATGGAAAGTATGAAAATTAAGCTTAAGCTGGAAGGGTCTTATGGGTGTATTTCAA 60
Db 217 ATGGAGAAGTATGAAAATTAAGCTTAAGCTGGAAGGGTCTTATGGGTGTATTTCAA 276
Qy 61 TGCAGAAACAAACCTCTGCACAAAGTAGTACTGTGTTAAAAATTTGGGAATCTGAAGAT 120
Db 277 TGTAGAAACAGGACACGGGTGAGATTGTGCCATCAAGAAGTTTCTGGAATCAGAAGAT 336
Qy 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACACAT 180
Db 337 GACCTGTCTAAGAAATTTGCCCTTTCGGGAAATCCGAATGCTCAAGCAACTCAAGAT 396
Qy 181 CCAATCTCTGTAACCTCATCGAGGTGTTTCAGGAGAAAGAAATGCAATTTAGTTT 240
Db 397 CCNACCTTGTTAACCTCTCGAAGTCTTCAGGAGGAAACGGAGGCTTCACCTGTGTT 456
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAAGTGTGAT 300
Db 457 GAATATTGTGACACACAGTTCTCCATGAGTTGGACAGATACCAAGAGGGGTACAGAA 516
Qy 301 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 517 CATCTCTGTAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTGGCATAAACAC 576
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATTAAGCAAGGAATATATC 420
Db 577 AATTGCATACATAGACAGCTGAAGCCAGAAATATCTCATCAGAAACATTCCTGTGAT 636
Qy 421 AAGATTGTGACTTTCGGGTTTGGCAAAATTTCTGATT---CCAGAGATGCTACACCGAT 477
Db 637 AAGCTTTGTGACTTTGGATTGTCTCGGCTTTTGAAGCCGAGTGTACTACTATACAGAC 696
Qy 478 TATGTAGCTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATACCTCAGTATGGT 537
Db 697 TACGTGGCTACCGAGTGGTACCGCTCCCTGAGCTGCTGTGGGGGACACGCGATAGCGC 756
Qy 538 TCTTCAGTCGATATATGGGCTATTTGGTTGTGTTTTCAGAGCTCTCTGACAGGCGCAGCA 597
Db 757 CCCCCTGGTATGTTTGGGCAATTTGGCTGTCTTTGCTGAGCTGCTGTGAGGAGTGCCT 816
Qy 598 CTGTGGCTTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAAA 657
Db 817 CTGTGGCCAGGAAATCGGATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGAT 876
Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATA 717


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; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5

Query Match      30.4%; Score 287; DB 16; Length 1701;
Best Local Similarity 59.1%; Pred. No. 8.7e-65;
Matches 510; Conservative 0; Mismatches 350; Indels 3; Gaps 1;

Qy 1 ATGGAAGAATGATGAAATTAAGCTAAGACTCGAGAAGGGTCTTATGGGGTTGTATTCAAA 60
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Qy 1 ATGGAAGAATGAGAACCTTGGATTGGTTGGAGAGGGAGTTATGGAATGATGAAG 60
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Qy 61 TCGAGAAACAAACCTCTGGACAAGTAGTACTGTGTTAAAAATTTGTGGAATCTGAAGAT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 TGTAGGAATAAAGATAGTGGGAAGAAATGTGGCCATCAAGAAGTTCTTAGAAAGTGATGAT 120
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Qy 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
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Qy 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAAAGAAATGCAATTTAGTTTTT 240
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Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
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Qy 241 GAAATTTGTGACCAACAGATTTCTGTAGTACTTGGAACTCTTTCCAAATGGACTAGATGAC 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 360
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Qy 301 CAAGTAGTTCAAAAGTATTGTTTTCAGATTAATTAATGGAATTTGTCACAGTCAC 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 361 AACTGTATTTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420
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Qy 361 AATATCATACATAGATATAAAGCCAGAGATATATTGGTCTCCAGTCTGGCGTTGTC 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Qy 421 AAGTTATGTGATTTTGGATTTGACCGGACACTGGCAGCTCCCGGAGAGGTTTACACTGAT 480
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Qy 478 TATGTAGCTAGAGATGATACCGAGCTCTGAACTTCTTGTGGGAGATACACTAGTATGCT 537
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Qy 481 TATGTGCAACTCGATGTACAGAGCTCCAGAACTACTGTTGGTGGTATGTCAGTATGGC 540
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Qy 538 TCTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTTGACAGGCCAGCCA 597
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Qy 541 AAAGCTGTGGATGTGGGCCATTTGGTTGCTGTGTAAGTGAATGCTCATGGGGGAACCC 600
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Qy 598 CTGTGGCTTGGAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAAACACTAGGAAA 657
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Qy 601 CTGTTTCTCGAGACTCTGATATTGATCAGCTTTTATCTTATTATGAGGTGTTAGGTAAT 660
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Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 717
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Qy 661 CTAATTCGAAGACACAGGAGCTTTTATATAAAATCCTGTGTTGTGGAGTAAGGTTG 720
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Qy 718 CCTGAGCCAGAAAGACATGGAACCTCTGAGGAAAAGTTCTCAGATGTTTCATCTGTGGCT 777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 721 CCTGAATCAAGGAATCAGAACCCTTTGAAGACGCTATCCCAAGCTCTCAGAAGTTGTG 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 778 CTGAACCTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACTGTGTTCCAA 837
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Qy 781 ATAGATTTAGCAAGAAATGCTTACATGTTGACCCAGACAAAAGGCCCTTCTGTGCTGAG 840
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Qy 838 CTCCTGGAGAGCTCCTACTTTGA 860
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Qy 841 CTCCTACACCATGATTTCTTTCA 863
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-766-691-11

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	945	100.0	945	4	US-09-671-050-11	Sequence 11, Appl
2	929	98.3	972	4	US-09-671-050-5	Sequence 5, Appl
3	839	88.8	1041	4	US-09-671-050-9	Sequence 9, Appl
4	823	87.1	1068	4	US-09-671-050-3	Sequence 3, Appl
5	507	53.7	1819	4	US-09-671-050-13	Sequence 13, Appl
6	454.4	48.1	561	4	US-09-671-050-1	Sequence 1, Appl
7	454.4	48.1	594	4	US-09-671-050-7	Sequence 7, Appl
8	415.4	44.0	1177	4	US-09-949-016-1681	Sequence 1681, Ap
9	287	30.4	1701	3	US-09-411-628-5	Sequence 5, Appl
10	287	30.4	1701	4	US-10-174-794-5	Sequence 5, Appl
11	287	30.4	3080	3	US-09-411-628-3	Sequence 3, Appl
12	287	30.4	3080	4	US-10-174-794-3	Sequence 3, Appl
13	283.8	30.0	1794	4	US-09-949-016-2083	Sequence 2083, Ap
14	171.8	18.2	903	2	US-08-874-347-9	Sequence 9, Appl
15	171.8	18.2	903	3	US-09-093-522-9	Sequence 9, Appl
16	163.4	17.3	1476	2	US-08-969-106-1	Sequence 1, Appl
17	163.4	17.3	1476	4	US-09-338-125-1	Sequence 1, Appl
18	163.4	17.3	1476	4	US-09-266-225D-13	Sequence 13, Appl
19	163.4	17.3	1635	4	US-09-417-197-112	Sequence 112, App
20	163.4	17.3	1635	4	US-09-417-197-114	Sequence 114, App
21	161.8	17.1	1296	4	US-09-949-016-2154	Sequence 2154, Ap
22	161.8	17.1	2213	4	US-09-023-655-1037	Sequence 1037, Ap
23	155.6	16.5	1050	4	US-09-220-132-3	Sequence 3, Appl
24	155.6	16.5	1825	4	US-09-919-039-115	Sequence 115, App
25	152.4	16.1	1042	4	US-09-949-016-4802	Sequence 4802, Ap
26	146.8	15.5	3823	4	US-09-949-016-4276	Sequence 4276, Ap
27	136.6	14.5	1158	4	US-09-949-016-4906	Sequence 4906, Ap

28 136.6 14.5 1161 4 US-09-023-655-1373 Sequence 1373, Ap
29 136.6 14.5 1161 4 US-09-949-016-181 Sequence 181, App
30 136.6 14.5 1825 4 US-09-620-312D-313 Sequence 313, App
31 134.6 14.2 987 4 US-09-949-016-5854 Sequence 5854, Ap
32 134.6 14.2 1089 1 US-08-154-915-1 Sequence 1, Appli
33 134.6 14.2 1089 2 US-08-464-517-37 Sequence 37, Appl
34 134.6 14.2 1089 2 US-08-246-361A-37 Sequence 37, Appl
35 134.6 14.2 1089 3 US-08-463-772-37 Sequence 37, Appl
36 134.6 14.2 1089 5 PCT-US93-09945-1 Sequence 1, Appli
37 131 13.9 993 4 US-09-248-796A-4323 Sequence 4323, Ap
38 131 13.9 1002 1 US-08-463-090B-3 Sequence 3, Appli
39 120.4 12.7 1044 4 US-09-248-796A-4325 Sequence 4325, Ap
40 117.2 12.4 1070 1 US-08-463-090B-5 Sequence 5, Appli
41 112.4 11.9 69909 4 US-09-949-016-13423 Sequence 13423, A
42 112 11.9 1308 4 US-09-801-861-4 Sequence 4, Appli
43 112 11.9 1308 4 US-10-224-562-4 Sequence 4, Appli
44 112 11.9 2203 4 US-09-801-861-1 Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-671-050-11
; Sequence 11, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 945
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-11

Query Match 100.0%; Score 945; DB 4; Length 945;
Best Local Similarity 100.0%; Pred. No. 6.8e-258;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCAAGATGAAAAATAGCTAGCTGGAAGAGGTCTTATGGGGTTGTTATTCAAA 60
Db 1 ATGCAAGATGAAAAATAGCTAGCTGGAAGAGGTCTTATGGGGTTGTTATTCAAA 60
Qy 61 TGCAGAAACAAACCTCTGGAACAAAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGAACAAAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATATAAACAAT 180
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Db 181 CCAATCTTGTGACCTCATCGAGTGTTCAGGAGAAAGAAATGCATTTAGTTT 240
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTCTCAT 300
Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTCTCAT 300

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QY 301 GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
DB 301 GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
QY 361 AACTGTATTTCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
DB 361 AACTGTATTTCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
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DB 421 AAGATTCTGATCTCGGCTTGGCAAAATCTGATTCAGAGAGATGCTTACACCGATTAT 480
QY 481 GTAGCTACGAGATGCTACCGAGCTCTGAACTTTCTTGGGAGATATCTCAGTATGGTTCT 540
DB 481 GTAGCTACGAGATGCTACCGAGCTCTGAACTTTCTTGGGAGATATCTCAGTATGGTTCT 540
QY 541 TCAGTTCGATATATGGGCTTATGGTTGTTTGGGAGATATCTCAGTATGGTTCT 600
DB 541 TCAGTTCGATATATGGGCTTATGGTTGTTTGGGAGATATCTCAGTATGGTTCT 600
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DB 601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGATTAATCAGAACACTAGGAAATTA 660
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QY 721 GAGCCAGAGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTATCTGTTGGCTCTG 780
DB 721 GAGCCAGAGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTATCTGTTGGCTCTG 780
QY 781 AACTTTCATGAAGGGTGTTCAAGATGAATCCAGATGACGATTAACTGTTCCTCAACTC 840
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QY 841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
DB 841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
QY 901 GAAGGAAGAACAGAGACGCGCAACAGGTACTTCCGCTCAAAAGT 945
DB 901 GAAGGAAGAACAGAGACGCGCAACAGGTACTTCCGCTCAAAAGT 945

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RESULT 2

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US-09-671-050-5
; Sequence 5, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 972
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-5

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Query Match 98.3%; Score 929; DB 4; Length 972;
Best Local Similarity 100.0%; Pred. No. 2.4e-253;

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Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGAAAGATATGAAAAATTTAGCTAAGACTGGAGAGAGGCTTATATGGGTTGTATTTCAAA 60
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QY 121 GATCCTCTGTTTAAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGAACAT 180
DB 121 GATCCTCTGTTTAAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGAACAT 180
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DB 181 CCAATCTTGTGAACCTCATCGAGGTTTTCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
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DB 241 GAATACCTGATCATACACTTTTAAATGAGTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
DB 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
QY 361 AACTGTATTTCAGAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
DB 361 AACTGTATTTCAGAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACCTTGGGTTTGCACAAATTTCTGATTCAGAGAGATGCTTACACCGATTAT 480
DB 421 AAGATTGTGACCTTGGGTTTGCACAAATTTCTGATTCAGAGAGATGCTTACACCGATTAT 480
QY 481 GTAGTACAGAGATGGTACCGAGCTCTGAACTTTCTGTTGGGAGATATCTCAGTATGGTTCT 540
DB 481 GTAGTACAGAGATGGTACCGAGCTCTGAACTTTCTGTTGGGAGATATCTCAGTATGGTTCT 540
QY 541 TCAGTTCGATATATGGGCTATTTGTTTGGAGAGCTCTGACAGGCTCTGACAGGCCAGCCACTG 600
DB 541 TCAGTTCGATATATGGGCTATTTGTTTGGAGAGCTCTGACAGGCTCTGACAGGCCAGCCACTG 600
QY 601 TGGCCTGGAAAAATCAGATGTGGACCACTTTATCTGATTAATCAGAACACTAGGAAAAATTA 660
DB 601 TGGCCTGGAAAAATCAGATGTGGACCACTTTATCTGATTAATCAGAACACTAGGAAAAATTA 660
QY 661 ATCCCAAGACATCAATCAATCTTTAAAGTAAAGGTTTTCATGGCATCAGTATACCT 720
DB 661 ATCCCAAGACATCAATCAATCTTTAAAGTAAAGGTTTTCATGGCATCAGTATACCT 720
QY 721 GAGCCAGAGACATGGAACCTTTGAGGAAAGTTCTCAGATGATGAATTAACCTGTTCCCAACTC 840
DB 721 GAGCCAGAGACATGGAACCTTTGAGGAAAGTTCTCAGATGATGAATTAACCTGTTCCCAACTC 840
QY 841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
DB 841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
QY 901 GAAGGAAGAACAGAGACGCGCAACAGGT 929
DB 901 GAAGGAAGAACAGAGACGCGCAACAGGT 929

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RESULT 3
US-09-671-050-9
; Sequence 9, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory

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; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-9

Query Match      88.8%; Score 839; DB 4; Length 1041;
Best Local Similarity 90.8%; Pred. No. 8.3e-228;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGGAAGAATGTAAGAAATAGCTAAGCACTGAGAAAGGCTCTATGGGTGTATTCAA 60
Db 1 ATGGAAGAATGTAAGAAATAGCTAAGCACTGAGAAAGGCTCTATGGGTGTATTCAA 60
Qy 61 TGCAGAAACAAACCTCTGGAACAAGTAGTAGCTGTAAAGAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGAACAAGTAGTAGCTGTAAAGAAATTTGGGAATCTGAAGAT 120
Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAAGCAATTCATTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAAGCAATTCATTAGTTTTT 240
Qy 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATCGAGTTGCTGAT 300
Db 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATCGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Qy 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTAATCACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTAATCACTAAGCAAGGAATATC 420
Qy 421 AAGATTGTGACTTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTGTGACTTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACCTCTTGTGGAGATACCTAGTATGGTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACCTCTTGTGGAGATACCTAGTATGGTCT 540
Qy 541 TCAGTCAGATATATGGGTATTTGGTGTGTTTTTTCAGAGCTTCCTGACAGCCAGCCACTG 600
Db 541 TCAGTCAGATATATGGGTATTTGGTGTGTTTTTTCAGAGCTTCCTGACAGCCAGCCACTG 600
Qy 601 TGGCCTGGAATACAGATGTGGCAACTTTATCTGATTAATCAACAACCT----- 650
Db 601 TGGCCTGGAATACAGATGTGGCAACTTTATCTGATTAATCAACAACCT----- 650
Qy 651 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 684
Db 651 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 684

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Db 721 GTAGCCTCTCAAAGTGTGGAATTAAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Qy 685 AAAAGTAACGGGTTTTTCCATGTCATCAGTATACCTGAGCCAGAGACATGAAACTCTT 744
Db 781 AAAAGTAACGGGTTTTTCCATGTCATCAGTATACCTGAGCCAGAGACATGAAACTCTT 840
Qy 745 GAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACCTCATGAAGGGGTGCTGAAG 804
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACCTCATGAAGGGGTGCTGAAG 900
Qy 805 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTCTGGAGACTCTCTACTTTGATTCT 864
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTCTGGAGACTCTCTACTTTGATTCT 960
Qy 865 TTTCAAGAGGCCCAATTTAAAGAAAGCAGCTAATGAAGAAAGAAACAGAGAGCGCAA 924
Db 961 TTTCAAGAGGCCCAATTTAAAGAAAGCAGCTAATGAAGAAAGAAACAGAGAGCGCAA 1020
Qy 925 CAGTACTTCCGCTCAAAAGT 945
Db 1021 CAGTACTTCCGCTCAAAAGT 1041

RESULT 4
US-09-671-050-3
; Sequence 3, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-3

Query Match      87.1%; Score 823; DB 4; Length 1068;
Best Local Similarity 90.6%; Pred. No. 2.9e-223;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGGAAGAATGTAAGAAATAGCTAAGCACTGAGAAAGGCTCTTATGGGTGTATTCAA 60
Db 1 ATGGAAGAATGTAAGAAATAGCTAAGCACTGAGAAAGGCTCTTATGGGTGTATTCAA 60
Qy 61 TGCAGAAACAAACCTCTGGAACAAGTAGTAGCTGTAAAGAAATTTGTGGAAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGAACAAGTAGTAGCTGTAAAGAAATTTGTGGAAATCTGAAGAT 120
Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAAGCAATTCATTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAAGCAATTCATTAGTTTTT 240
Qy 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATCGAGTTGCTGAT 300
Db 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATCGAGTTGCTGAT 300

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QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACCTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACCTTCAAGCTCTTAATTTCTGTCAATACAT 360
QY 361 AACTCTATTTCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
Db 361 AACTCTATTTCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
QY 421 AAGATTGTGACTTCGGGTTTGGCAAAATCTGTGATTCAGAGATGCGCTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGGCAAAATCTGTGATTCAGAGATGCGCTACACCGATTAT 480
QY 481 GTAGCTACGAGATGTCAGAGCTTCTGAACTTCTTGTGGGAGATACCTAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGTCAGAGCTTCTGAACTTCTTGTGGGAGATACCTAGTATGGTTCT 540
QY 541 TCAGTTCGATATATGGGCTATTGGTTGTGTTTTCAGAGCTCTTGAAGGCGAGCACTG 600
Db 541 TCAGTTCGATATATGGGCTATTGGTTGTGTTTTCAGAGCTCTTGAAGGCGAGCACTG 600
QY 601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGATTAATCAGAACACTAGTAGAGAG 660
Db 601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGATTAATCAGAACACTAGTAGAGAG 660
QY 651 ----- 650
Db 651 ----- 650
QY 661 GGGTTTCGCCATGTTGACAGGCTGTTCTCGAACTCTTGGAGTCAAGTGATCCACCTGCC 720
Db 661 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 684
QY 651 ----- 684
Db 721 GTAGCCTCTCAAAGTCTGGAATACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
QY 685 AAAAGTAACGGGTTTCCATGGCATCAGTATACCTGAGCAGAGATGGAACCTCTT 744
Db 781 AAAAGTAACGGGTTTCCATGGCATCAGTATACCTGAGCAGAGATGGAACCTCTT 840
QY 745 GAGGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACTTTCATGAAGGGTGTCTGAAG 804
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACTTTCATGAAGGGTGTCTGAAG 900
QY 805 ATGAATCCAGATGACAGATTAACCTGTTCCTCAACTCTCTGAGAGCTCCTACTTTGATTCT 864
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCTCAACTCTCTGAGAGCTCCTACTTTGATTCT 960
QY 865 TTTCAAGGCGCCAAATTAAGAAAGCAGTATGAGGAAAGAAACAGAGAGCGCAA 924
Db 961 TTTCAAGGCGCCAAATTAAGAAAGCAGTATGAGGAAAGAAACAGAGAGCGCAA 1020
QY 925 CAGGT 929
Db 1021 CAGGT 1025

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RESULT 5
US-09-671-050-13
; Sequence 13, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-13

Query Match 53.7%; Score 507; DB 4; Length 1819;
Best Local Similarity 69.8%; Pred. No. 1.6e-133;
Matches 929; Conservative 0; Mismatches 0; Indels 402; Gaps 2;

QY 1 ATGCAAAAGTATGAAATTTAGCTTAACACTGGAGAGGGTCTTATGGGTTGTATTTCAAA 60
Db 138 ATGCAAAAGTATGAAATTTAGCTTAACACTGGAGAGGGTCTTATGGGTTGTATTTCAAA 197
QY 61 TGCAGAAACAAAACCTCTCGACAAAGTAGTAGCTTTAAAAAATTTGTGGAAATCTGAAGAT 120
Db 198 TGCAGAAACAAAACCTCTCGACAAAGTAGTAGCTTTAAAAAATTTGTGGAAATCTGAAGAT 257
QY 121 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 180
Db 258 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 317
QY 181 CCAATCTCTGAACTCTCATCGAGGTTTCCAGAGAAAGGAAATGCAATTTAGTTTTT 240
Db 318 CCAATCTCTGAACTCTCATCGAGGTTTCCAGAGAAAGGAAATGCAATTTAGTTTTT 377
QY 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCAATGGAGTTGCTGAT 300
Db 378 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCAATGGAGTTGCTGAT 437
QY 301 GAGTGATCAAAAGCGTATTATGGCAACACTTTCAAGCTCTTAAATTTCTGTCAATACAT 360
Db 438 GAGTGATCAAAAGCGTATTATGGCAACACTTTCAAGCTCTTAAATTTCTGTCAATACAT 497
QY 361 AACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
Db 498 AACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 557
QY 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTG----- 453
Db 558 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGAGTTGGACTTCATCTTCTCTGTGTGCC 617
QY 454 ----- 453
Db 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAAATTTCTTCTGCCAATTCAGAGATTTT 677
QY 454 ----- 453
Db 678 CTCTGCTTGGATCCATTCTGCACACAGTGTGTTTACCATTGGGGCCAGGCTCATCTCGA 737
QY 454 ----- 453
Db 738 ACTTCTGGCCTCAAGTATCTTCCACCTCGGCTCCCAAGTGTCTGGATTGCAAGTGTG 797
QY 454 ----- 453
Db 798 AGCCACCGTCCAGCCAGATTTTTCAAACAATACTACTGAGAGCTCAAGAGTTGTTT 857
QY 454 -----ATTCCAGAGATGCTTACACC 474
Db 858 TTAGTGGGAACACAAATTTTCGAACAAATTTCTTGAAAGCGCATTTCCAGAGATGCTTACACC 917
QY 475 GATTATGTAGCTACGAGATGTTACCGAGCTCTCGAACTTCTTGTGGGAGATACCTAGTAT 534
Db 918 GATTATGTAGCTACGAGATGTTACCGAGCTCTCGAACTTCTTGTGGGAGATACCTAGTAT 977
QY 535 GGTTCCTTCAGTTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCTCTGACAGCCAG 594
Db 978 GGTTCCTTCAGTTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCTCTGACAGCCAG 1037
QY 595 CCACTGTGCGCTGGAAATATCAGATGTGGACCAATTTATCTGTATATCAAGACACTT----- 650

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Db 1038 CCACTGTGGCCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATATCAGAACACTAGTA 1097
Qy 651 ----- 650
Db 1098 GAGACGGGGTTTCGCCATGTTGACCGGTGGTCTCGAACTCTTGACGTCAAAGTGATCCA 1157
Qy 651 -----AGGAAAAATTAATCCCAAGACATCA 678
Db 1158 CTTGCCCTGACCTCTCAAAGTGTGGAATTAACAGGAAAAATTAATCCCAAGACATCA 1217
Qy 679 ATCTTTAAAAAGTAACCGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATCGAA 738
Db 1218 ATCTTTAAAAAGTAACCGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATCGAA 1277
Qy 739 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTGTGCTCTGAACTTCATGAAGGGGTGT 798
Db 1278 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTGTGCTCTGAACTTCATGAAGGGGTGT 1337
Qy 799 CTGAGATGATCCAGATGACAGATTAACTGTTCCCAACTCTCTGGAGAGCTCTACTTT 858
Db 1338 CTGAGATGATCCAGATGACAGATTAACTGTTCCCAACTCTCTGGAGAGCTCTACTTT 1397
Qy 859 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCACGTATGAAGGAAGAAACAGAGA 918
Db 1398 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCACGTATGAAGGAAGAAACAGAGA 1457
Qy 919 CGCCAACAGGT 929
Db 1458 CGCCAACAGGT 1468

RESULT 6

US-09-671-050-1
; Sequence 1, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-1

Query Match 48.1%; Score 454.4; DB 4; Length 561;
Best Local Similarity 99.8%; Pred. No. 7.5e-119;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGAAGAAGTATGAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
Db 1 ATGGAAGAAGTATGAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Qy 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAAGACAT 180
Db 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAAGACAT 180
Qy 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCCAAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCCAAAATGGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360

Qy 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCCAAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCCAAAATGGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Qy 361 AACTGTATTTCACAGAGATATAAAACCTGGAATAATTTCTTAATACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTTCACAGAGATATAAAACCTGGAATAATTTCTTAATACTAAGCAAGGAATAATC 420
Qy 421 AAGATTGTGACTTTCGGGTTTGACAAAAATTTCTGATT 456
Db 421 AAGATTGTGACTTTCGGGTTTGACAAAAATTTCTGATT 456

RESULT 7

US-09-671-050-7
; Sequence 7, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-7

Query Match 48.1%; Score 454.4; DB 4; Length 594;
Best Local Similarity 99.8%; Pred. No. 7.8e-119;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGAAGAAGTATGAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
Db 1 ATGGAAGAAGTATGAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Qy 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAAGACAT 180
Db 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAAGACAT 180
Qy 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCCAAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCCAAAATGGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360

Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
 QY 361 AACTGTATTACAGAGATATAAACCCTGAATATTTCTAAATATTAAGCAAGGATATATC 420
 Db 361 AACTGTATTACAGAGATATAAACCCTGAATATTTCTAAATATTAAGCAAGGATATATC 420
 QY 421 AAGATTTCGTGACTTCGGGTTTGCAAAATTTCTGATT 456
 Db 421 AAGATTTCGTGACTTCGGGTTTGCAAAATTTCTGATT 456

RESULT 8

US-09-949-016-1681
 ; Sequence 1681, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1681
 ; LENGTH: 1177
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-1681

Query Match 44.0%; Score 415.4; DB 4; Length 1177;
 Best Local Similarity 66.7%; Pred. No. 1.3e-107;
 Matches 609; Conservative 0; Mismatches 301; Indels 3; Gaps 1;
 QY 1 ATGCAAAAGATGAAAATTAAGCTTAAGACTGGAGAGGGCTTATGGGTTGATTCAAA 60
 Db 32 ATGCAAGATGAAAATTAAGCTTAAGACTGGAGAGGGCTTATGGGTTGATTCAAA 91
 QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTCTTAAATAATTTGGGAATCTGAAGAT 120
 Db 92 TGTAGAACAGGACACGGGTGAGTGTGGCCATCAAGAGTTCTTGAATCAGAGAT 151
 QY 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db 152 GACCTGTCTATAAGAAATATGCGCTTTCGGGAAATCGGAATGCTCAAGCAACTCAAGCAT 211
 QY 181 CCAATCTGTGACCTCATCGAGTCTTCCAGGAAAGGAAATGCAATTTAGTTT 240
 Db 212 CCNACCTGTTTACCTCTCGAAGTCTTCCATGAGTTGGACAGATACCAAGAGGGTACAGAA 271
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
 Db 272 GAATATTGTGACACACAGTTCTCCATGAGTTGGACAGATACCAAGAGGGTACAGAA 331
 QY 301 GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
 Db 332 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGAAATTTTGGCATAAACAC 391
 QY 361 AACTGTATTACAGAGATATAAACCCTGAATATTTCTAATACTAAGCAAGGATATATC 420
 Db 392 AATTGCATATAGACGTTGACCGCAGAAATATCTCTCATCAGAAACATTCGCGATT 451
 QY 421 AAGATTTCGTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGGAGATGCTTACACCGAT 477
 Db 452 AAGCTTTGTGACTTTGGATTGCTCGGCTTTTGACTGGACCGAGTGACTACTATACAGAC 511
 QY 478 TATGTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGAGATACCTAGTATGGT 537

Db 512 TACGTGCTACCAAGTGTATCCGCTCCCTGAGCTGCTGGTGGGGACACGCGATACGGC 571
 QY 538 TCTTCAGTCGATATATGCGGCTATTGGTGTGTTTTTGCAGAGCTCTTGACAGGCGACCCA 597
 Db 572 CCCCGGTGATGTTTGGCAATTTGGCTGTGCTCTTTGCTGAGCTGCTGTGAGGAGTGCCT 631
 QY 598 CTGTGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATATCAAGAACACTAGGAAAA 657
 Db 632 CTGTGGCCAGGAAATCGAATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGGAT 691
 QY 658 TTAATCCAAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATA 717
 Db 692 CTCATTCTTAGGCACAGCAAGTGTGTAGCACGAATCAGTACTTTCAGTGAGTGAATTT 751
 QY 718 CTTGAGCCAGAACATGGAACCTCTTTGAGGAAAAAGTTTCTCAGATGTTCTATCTCTGCTG 777
 Db 752 CCAGACCTGAAGATATGGAACCACTTGAATTTAAATTTCCAAACATCTCTTATCTCTGCC 811
 QY 778 CTGAACTTCTGAGAGGGTCTCTGAAGATGAATCCAGATCAGATCAAGATTAACTGTTCCTCAA 837
 Db 812 CTGGGGCTCTTAAAGGGCTGTCTCCACATGAGCCCTACTGAAAAGGCTGACATGTGAACAG 871
 QY 838 CTCCTGGAGAGCTCTTACTTTTGAATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGT 897
 Db 872 CTGTTGATCACCCTATTTTGAACATCAGAGAAATAGAGGATTTGGCAAGAACAC 931
 QY 898 AATGAAGAAAGAA 910
 Db 932 AACAAACCAACAA 944

RESULT 9

US-09-411-628-5
 ; Sequence 5, Application US/09411628
 ; Patent No. 6428994
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
 ; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/09/411,628
 ; CURRENT FILING DATE: 1999-10-01
 ; EARLIER APPLICATION NUMBER: US 60/102,906
 ; EARLIER FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1701
 ; TYPE: DNA
 ; ORGANISM: Orcytolagus cuniculus
 US-09-411-628-5

Query Match 30.4%; Score 287; DB 3; Length 1701;
 Best Local Similarity 59.1%; Pred. No. 4e-71;
 Matches 510; Conservative 0; Mismatches 350; Indels 3; Gaps 1;
 QY 1 ATGGAAGATGTAATAAATAGCTAAGACTGGAGAGGGCTTATCGGGTTGATTCAAA 60
 Db 1 ATGGAAGATGTAATAAATAGCTAAGACTGGAGAGGGCTTATCGGGTTGATTCAAA 60
 QY 61 TGCAGAAACAAACCTCTCGCAAGTAGTAGCTGTTTAAAAAATTTCTGGAATCTGAAGAT 120
 Db 61 TGTAGGAATTAAGATAGTAGTAGAGGATTTGGCCATCAAGAGTTCTTAGAAGTATGAT 120
 QY 121 GATCTGTTGTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db 121 GACAAATGTTTAAAAAATTTGCTATCGAGAAATCAAGTTACTTAAAGCAACTGAGGCAT 180
 QY 181 CCAATCTTGTGAACCTCATCGAGGTTTTCAGGAGAAAGGAAATGCAATTTAGTTT 240
 Db 181 GAAATTTGTGATCTGTTGGAGGTTGTAAAAAAGGATGATGTTACCTAGTCTTT 240

241	Qy	GAATACTGTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGTGAT	300
241	Db		
241	Qy	GAATTTGTTGTGCCACACAGATTTCTTGATGACTTTGGAACTCTTTCCAAATGGACTAGATGAC	300
241	Db		
301	Qy	GGAGTGTATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT	360
301	Db		
301	Qy	CAAGTAGTTTCAAAAGTATTGTTCAGATTATTAAATGGAAATGGATTTTGTTCACAGTCAAC	360
301	Db		
361	Qy	AACGTGATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAGCAAGGAATAATC	420
361	Db		
361	Qy	AATATCATACATAGAGATATAAAGCCAGAGAATATTTGGTCTCCAGTCTGGCGTTGTC	420
361	Db		
421	Qy	AAGATTGTGTGACTTCGGGTTTGGCAAAATTTCTG ---ATTCCAGGAGATGCCCTACACCGAT	477
421	Db		
421	Qy	AAGTTATGTGTGATTTTGGATTTTGCACGGACACTGGCAGCTCCGGAGAGGTTTACACTGAT	480
421	Db		
478	Qy	TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTTCTTGGGAGATACTCAGTATGTT	537
478	Db		
481	Qy	TATGTGGCAACTCGATGGTACAGAGCTCCAGAACTACTGTTGGTGATGTCAAGTATGGC	540
481	Db		
538	Qy	TCCTTCAGTTCGATATATANGGCTATTGGTGTGTTTTTGGCAGAGCTCCTGACAGGCCAGGCA	597
538	Db		
541	Qy	AAAGCTGTGGATGTGTGGGCCATTGGTTGTCTGGTAACTGTAATGCTCATGGGGGAAACC	600
541	Db		
598	Qy	CTGTGGCTCGAAATCAGATGCTGGACCAACTTTTATCTGATAATCAGAACACTAGGAAAA	657
598	Db		
601	Qy	CTGTTCTCGGAGACTCTGATATTGATCAGCTTTATCTTATATGAGTGTTTTAGTAAAT	660
601	Db		
658	Qy	TTAATCCACAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATA	717
658	Db		
661	Qy	CTAATTCCAAGACACCAGGAGCTTTTATATAAAATCTGTGTTTGTGGAGTAAGGTTG	720
661	Db		
718	Qy	CCTGAGCCAGAAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGTTTCATCTCTGTGCT	777
718	Db		
721	Qy	CCTGAAATCAAGGAATCAGAAACCTCTTGAAGACGCTATCCCAAGCTCTCAGAAGTTTGTG	780
721	Db		
778	Qy	CTGAACTTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAA	837
778	Db		
781	Qy	ATAGATTTAGCAAGAAATGCTTACATGTTGACCCAGACAAAAGGCCCTTCTGTGCTGAG	840
781	Db		
838	Qy	CTCCTGGAGAGCTCCTACTTTGA 860	
838	Db		
841	Qy	CTCCTACACCATGATTTCTTTCA 863	
841	Db		

RESIT.T 10

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US-10-174-794-5
; Sequence 5, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: cDNA, GENOMIC, AND PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5

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Query Match
30.4%; Score 287; DB 4; Length 1701;

Best Local Similarity 59.1%; Pred. No. 4e-71;

Best local similarity	Seq. no.	Seq. no.	Seq. no.
Matches 510; Conservative	0; Mismatches 350; Indels	3; Gaps	1;

QY 1 ATGGAAGAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAA 60

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RESULT 11
US-09-411-628-3
; Sequence 3, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02

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Qy 598 CTGTGGCTCGAAATCAGATGTGGACCAACTTTATCTGTAATCAACAGAACTAGGAAA 657
Db 849 CTGTTCTCTGGAGACTCTGATATTGATCAGCTTTTATCTTATTATGAGGTGTTAGTAAT 908
Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 717
Db 909 CTAATTCGAACACACGAGGAGCTTTTATATAAAATCCTGTGTTTCTGGAGTAAGTTG 968
Qy 718 CCTGAGCCAGAGACATGGAACCTTTTGAGGAAAAGTTCTCAGATGTTCAFCCTGTGGCT 777
Db 969 CCTGAAATCAAGGAATCAGAACCTTTTGAAGACGCTATCCAGCTCTCAGAAAGTTGTG 1028
Qy 778 CTGAACCTTCATGAAGGGTGTCTGAAGATGAATCCAGATCAGATTAACCTGTTCCAA 837
Db 1029 ATAGATTAGCAAGAAATGCTTACATGTTGACCCAGACAAAAGGCCCTTCTGTGCTGAG 1088
Qy 838 CTCCTGAGAGCTCCTACTTTGA 860
Db 1089 CTCCTACCATGATTTCTTTCA 1111

RESULT 13
US-09-949-016-2083
; Sequence 2083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2083
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2083

Query Match 30.0%; Score 283.8; DB 4; Length 1794;
Best Local Similarity 58.9%; Pred. No. 3.3e-70;
Matches 508; Conservative 0; Mismatches 352; Indels 3; Gaps 1;

Qy 1 ATGGAAAGTATGAAAATTAAGCTAAGACTGGAGAGGCTTATGGGGTTGTATTCAAA 60
Db 376 ATGGAAAATATGAAAACCTCGGTTTGGTTGAGAGGGAGTTATGGAATGGTATGAG 435
Qy 61 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 436 TGTAGGAATAAGATACTGGAAGAATTTGTGCCCAATAAGAAAGTTCTTAGAAAGTGACGAT 495
Qy 121 GATCCTGTTTAAAGAAATAGCACTAAGACAAATACGTATGTTGAAGCAATTAACAT 180
Db 496 GACAAAATGGTTAAAGAAATTTGCAATGCGAGAAATCAAGTTACTAAAGCAACTTAGGCAT 555
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 556 GAAACTTGTGGAATCTCTTGGAGTGTGTGAAGAAAACCAATGTTACCTAGTCTTT 615
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCAAAATGGAGTTGCTGAT 300
Db 616 GAAATTTGTTGACCAACAATTTCTTGAAGTGTGAGCTCTTTCAAATGGAGTAGACTAC 675
Qy 301 GGAGTGATCAAAAGGGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCTATACAT 360
Db 676 CAAGTAGTTCAAAAAGTATTTGTTTTCAGATTATTAATGAATTTGATTTTGTACAGTCAC 735

Qy 361 AACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATATATC 420
Db 736 AATATCATACACAGAGATATAAAGCCAGAGAAATATATTAGTCTCCAGTCTGGGGTTGTC 795
Qy 421 AAGATTGTGACTCGGGTTTGCAAAATCTG---ATTCCAGGAGATCCCTACACCGAT 477
Db 796 AAGCTATGCGATTTTGGATTTGCGCGAAACATTGGCAGCTCCTGGGAGGTTTATACTGAT 855
Qy 478 TATGTACTACGAGATGGTACCCGAGCTCCTGAACTTCTTGTGGGAGATCTCAGTATGGT 537
Db 856 TATGTGCAACCCGATGGTACAGAGCTCCAGAACTATTGGTTGGTGTGATGTCAGTATGSC 915
Qy 538 TCTTCAGTCATATATGGCTATTGGTTGTGTTTTCAGAGCTCCTGACAGGCCAGCCA 597
Db 916 AAGGCTCTGTATGTGTGGCCATTGGTTGTCTGTAACGAAATGTTTCATGGGGGAACCC 975
Qy 598 CTGTGGCTCGAAAATCAGATGTGGCAACAACTTTTATCTGATAATCAGAACACTAGGAAA 657
Db 976 CTATTTCTGGAGATCTGATATTGATCAGCTATATATATTATGATGTGTTTAGTAT 1035
Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 717
Db 1036 CTAATTCAGGCAATCAGGAGCTTTTATAAATAATCCTGTGTTTCTGGAGTAAGTTG 1095
Qy 718 CTGAGCCAGAAAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGTTTCATCCTGTGCT 777
Db 1096 CCTGAAATCAAGGAAAGAGAAACCTCTTTGAAAAGACGCTATCTTAAGCTCTCTGAAAGTGGTG 1155
Qy 778 CTGACTTCATGAGGGGTTCTGAAGATGAATCCAGATCAGATGACAGATTAACTGTTCCAA 837
Db 1156 ATAGATTAGCAAGAAATGCTTACATATTGACCCCAAGAACCCCTTCTGTGCTGAG 1215
Qy 838 CTCCTGAGAGCTCCTACTTTGA 860
Db 1216 CTCCTACCATGATTTCTTTCA 1238

RESULT 14
US-08-874-347-9
; Sequence 9, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,347
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696

QY		832	TCCCAACTCCTGGAGAGCTCCTACTTCTGATTCCTTT	866
Db		835	AAAAAGACTCTGCATCATCCTTATTTCGTGATTT	869
RESULT 15				
US-09-093-522-9				
; Sequence 9, Application US/09093522				
; Patent No. 6015700				
; GENERAL INFORMATION:				
; APPLICANT: Lamper, Andrew H.				
; APPLICANT: Leof, Edward B.				
; APPLICANT: Thomas, Charles F.				
; APPLICANT: Gustafson, Michael P.				
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS				
; TITLE OF INVENTION: CARINII				
; NUMBER OF SEQUENCES: 26				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Fish & Richardson P.C., P.A.				
; STREET: 60 South Sixth Street, Suite 3300				
; CITY: Minneapolis				
; STATE: MN				
; COUNTRY: USA				
; ZIP: 55402				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: Diskette				
; COMPUTER: IBM Compatible				
; OPERATING SYSTEM: DOS				
; SOFTWARE: Fast-Seq for Windows Version 2.0				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/09/093,522				
; FILING DATE: 08-JUN-1998				
; CLASSIFICATION:				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: 08/874,347				
; FILING DATE: 13-JUN-1997				
; ATTORNEY/AGENT INFORMATION:				
; NAME: Ellinger, Mark S.				
; REGISTRATION NUMBER: 34,812				
; REFERENCE/DOCKET NUMBER: 07039/055002				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: 612-335-5070				
; TELEFAX: 612-288-9696				
; TELEX:				
; INFORMATION FOR SEQ ID NO: 9:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 903 base pairs				
; TYPE: nucleic acid				
; STRANDEDNESS: single				
; TOPOLOGY: linear				
; MOLECULE TYPE: cDNA				
; FEATURE:				
; NAME/KEY: Coding Sequence				
; LOCATION: 1...900				
; OTHER INFORMATION:				
US-09-093-522-9				
Query Match			18.2%;	Score 171.8; DB 3; Length 900
Best Local Similarity			52.3%;	Pred. No. 1.4e-38;
Matches 458; Conservative			0; Mismatches 402;	Indels
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QY		61	TGCAGAACAAAAACCCTCTGCACAAGTAGTAGCTGTTAAABAAAATTTTGTGCA	
Db		61	GCAAAGGATCTTGAAGTGTTACAAATTGTAGCTCTTTAAGAAATTCGATT	
QY		121	GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCA	
Db		121	GATGAGGGAGTTCCTAGTACAGCAAATTCGTGAGATATCACTTTTGAAGCA	

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Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTCAAGGAGAAAAGGAAAATGCATTTAGTTTTT 240
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181 GATAATGTTGTAAGACTTTTGAATATAATTTCATCAAGAGTCACGTTTATATCTTGTGTTTT 240
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATG-----GAGTT 294
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 GAATTTCTTGATCTTGATTTAAAAGAGTATATGATATGTTCCAAAGGACATGTCCTT 300
Qy 295 GCTGATGAGTGATCAAAAGCGTATTATGGCAACACCTTCAAGCTCTTAAATTTCTGTGCAT 354
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 GGTGAGAAATGATTAAAAGTTTATGTGCACAACTTGTATCAGGTGTTAAATATTGTCAT 360
Qy 355 ATACATACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTTAAGCAAGGA 414
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 TCTCATCGTATTCTTCATCGTGACTTGAACACCAAAATCTTCTATAGATCGAGAAGGA 420
Qy 415 ATAATCAAGATTTGTGCTTCGGGTTTGCA---CAAATTCGTATCCAGGAGATGCCTAC 471
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AATCTTAAATTAGCAGATTTTGGGCTTGCAAGGGGTTTGGTGTCCATTCGGTGGTTAT 480
Qy 472 ACCGATTATGATGATGAGATGTCAGAGCTCTGAACTTCTTGTGGGAGATACACTCAG 531
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 ACTCATGAGTTGTTACACTTTGGTATCGTCTCAGAGTTCTTTAGGTGGTCGACAA 540
Qy 532 TATGGTTCTTCAGTCGATATATGGGCTATTTGGTTGTGTTTTTGAGAGCTCCTGCACAGGC 591
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 TATGCAACAGCGCTTGATATATGAGCATTTGGATGTATTTTTCAGAAATGGCTACAAA 600
Qy 592 CAGCCACTGTGGCTTGGAAATCAGATGTGACCAACTTTATCTGATAATCAGAACACTA 651
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 AAGCCATTATTTCCAGGTGATTTGAAATTTGATGAAATATTTAGAAATATTTAGAAATTA 660
Qy 652 GGAATAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATC 711
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
661 GGGACTCCAGATGAAATTTCTTGGCTGGTATTACATCTTATCCGGATTTTAAGGCACT 720
Qy 712 AGTATACCTGAGCCAGAGACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTTCATCCT 771
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721 TTTCCAAAATGGTCACCA-----AAAAATCTTGAGAAATTAATTACAGAACTTGCATAGT 774
Qy 772 GTGGCTCTGAACTTCATGAAGGGGTGCTGAAGATGATCCAGATGACAGATTAAACCTGT 831
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
775 GATGGAATAGATTTATTACAGAAATGCTTAGATATTATCTCTGTAACGTTAGCGCT 834
Qy 832 TCCCAACTCCTGGAGAGCTCCTACTTTGATTTCTTT 866
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
835 AAAAAAGCTCTCGATCATCCTTATTTTGTGATTT 869

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Search completed: April 22, 2005, 01:29:34
Job time : 183.912 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:23:24 ; Search time 517.228 Seconds
(without alignments)
10815.645 Million cell updates/sec

Title: US-10-766-691-11

Perfect score: 945
Sequence: 1 atggaagatgataaaatt.....aggacttcgcgtcaaaagt 945

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	4	AAD03817 Human kin
2	929	98.3	972	4	AAD03814 Human kin
3	927	98.1	1790	6	AAD30557 Human kin
4	868.8	91.9	1678	10	ABX08936 cDNA enco
5	863	91.3	1083	4	AA06725 Polynucle
6	839	88.8	1041	4	AAD03816 Human kin
7	823	87.1	1068	4	AAD03813 Human kin
8	808	85.5	1266	12	ADK71927 Human kin
9	704.4	74.5	1429	12	ADI40928 Human kin
10	645.4	68.3	882	6	AAI64248 Human kin
11	643	68.0	911	4	AAF44669 Novel pro
12	643	68.0	911	12	ADI29367 Human MAR
13	559.2	59.2	2615	4	AAF44670 Novel pro
14	559.2	59.2	2615	12	ADI29368 Mouse MAR
15	543.2	57.5	1281	8	ABX34679 Human mdd
16	507	53.7	1819	4	AAD03818 Human kin
17	501	53.0	1086	10	ABZ77165 Human pro
18	454.4	48.1	561	4	AAD03812 Human kin
19	454.4	48.1	594	4	AAD03815 Human kin
20	415.4	44.0	1612	6	ABQ93433 Human CDN

21	413.8	43.8	1175	12	ADO01536	Ado01536 Human cys
22	413.8	43.8	1178	12	ADO01535	Ado01535 Human cys
23	413.8	43.8	2944	5	ABV24584	Abv24584 Human pro
24	287	30.4	1698	3	AAA29746	Aaa29746 Rabbit KK
25	287	30.4	3080	3	AAA29745	Aaa29745 Rabbit KK
26	283.8	30.0	2095	10	ADC77658	Adc77658 Human 162
27	283.8	30.0	2095	13	ADQ89155	Adq89155 Human uro
28	274	29.0	1179	4	ABL12603	Ab112603 Drosophil
29	227.4	24.1	1513	3	AAZ51208	Aaz51208 Human los
30	227.4	24.1	1513	12	ADI57213	Adi57213 Human NKI
31	227.4	24.1	1773	4	AA06724	Aa06724 Polynucle
32	218.4	23.1	3297	4	ABL12602	Ab112602 Drosophil
33	215.8	22.8	2503	13	ACN42574	Acn42574 Human dia
34	211.4	22.4	1667	3	AAZ51207	Aaz51207 Rat lost
35	211.4	22.4	1738	3	AAZ51206	Aaz51206 Rat lost
36	177.4	18.8	1158	5	AA070329	Aa070329 DNA enco
37	175.8	18.6	1866	4	AAF44672	Aaf44672 Novel pro
38	175.8	18.6	1866	12	ADI29370	Adi29370 Human MAR
39	171.8	18.2	903	2	AA07476	Aa07476 Pneumocys
40	171.4	18.1	2982	12	ADO01537	Ado01537 Human cys
41	163.4	17.3	1476	3	AAZ37835	Aaz37835 Cyclin-de
42	163.4	17.3	1635	2	AAV71074	Aav71074 Green flu
43	163.4	17.3	1635	2	AAV71073	Aav71073 CDK2-gree
44	163	17.2	1024	10	AB283372	Ab283372 Toxicolog
45	163	17.2	1297	6	ABQ60787	Abq60787 Human 10C

ALIGNMENTS

RESULT 1
AAD03817
ID AAD03817 standard; cDNA; 945 BP.

AC AAD03817;

DT 19-JUN-2001 (first entry)

DE Human kinase cDNA #6.

KW Human; kinase; gene therapy; bioreactor; mental disorder;
biological disorder; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..945

FT /product= "Human kinase #6"

FT /note= "The coding region does not include stop codon"

FT /partial

PN WO200123579-A1.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026621.

XX 28-SEP-1999; 99US-0156511P.

XX (LEXI-) LEXICON GENETICS INC.

PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;

PI Sands AT;

XX WPI; 2001-266166/27.

XX P-PSDE; AAE00495.

PT New isolated human kinase polynucleotide useful for generating
antibodies, as reagents in diagnostic assays and for screening for
compounds useful for treating mental, biological or medical diseases.

XX Claim 3; Page 33; 38pp; English.

PS

The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinases, the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioeffectors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 945 BP; 323 A; 165 C; 202 G; 255 T; 0 U; 0 Other;

Query Match 100.0%; Score 945; DB 4; Length 945;
Best Local Similarity 100.0%; Pred. No. 3.3e-244;
Matches 945; Conservative 0; Mismatches 0; Indels

Qy	1	ATGAAAAGATGATGAAAAATTAAGCTAAGACTGGAGAAGGCTTTATGGGGTTGTATTCAAA	60
Db	1	ATGAAAAGATGATGAAAAATTAAGCTAAGACTGGAGAAGGCTTTATGGGGTTGTATTCAAA	60
Qy	61	TGCAGAAACAAAACCTCTGGACAAGTAGTACTGCTTAAAAAATTTGTGGAATCTGAAGAT	120
Db	61	TGCAGAAACAAAACCTCTGGACAAGTAGTACTGCTTAAAAAATTTGTGGAATCTGAAGAT	120
Qy	121	GATCCTGTGTTTAAAGAAAAATAGCACTAAGAGAAATACGTATGTTTGAAGCAATTA AAAACAT	180
Db	121	GATCCTGTGTTTAAAGAAAAATAGCACTAAGAGAAATACGTATGTTTGAAGCAATTA AAAACAT	180
Qy	181	CCAAATCTGTGAACTTCATCGAGTCTTCAGGAGAAAAGGAAAAATGCAATTAGTTTTTT	240
Db	181	CCAAATCTGTGAACTTCATCGAGTCTTCAGGAGAAAAGGAAAAATGCAATTAGTTTTTT	240
Qy	241	GAATACTGTGATCATACACATCTTTAAATGAGCTGGAAGAAAAACCAAAATGAGTGTCTGAT	300
Db	241	GAATACTGTGATCATACACATCTTTAAATGAGCTGGAAGAAAAACCAAAATGAGTGTCTGAT	300
Qy	301	GGAGTGCATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT	360
Db	301	GGAGTGCATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT	360
Qy	361	AACCTGTATTCACAGAGATATAAAAACCTCGAAAAATTTCTAATAACTAAGCAAGGAATAATC	420
Db	361	AACCTGTATTCACAGAGATATAAAAACCTCGAAAAATTTCTAATAACTAAGCAAGGAATAATC	420
Qy	421	AAGATTGTGACHTTCGGGTTTGCAAAATCTGATTCACAGAGATGCTTACACCGATTAT	480
Db	421	AAGATTGTGACHTTCGGGTTTGCAAAATCTGATTCACAGAGATGCTTACACCGATTAT	480
Qy	481	GTAGCTACGAGATGGTACCGAGCTCTCGAACTTTCTGTGGGAGATACCTAGTATGGTCT	540
Db	481	GTAGCTACGAGATGGTACCGAGCTCTCGAACTTTCTGTGGGAGATACCTAGTATGGTCT	540
Qy	541	TGAGTCGATATATGGGCTATTGGTTGTGTTTTGCGAGCTCTCTGACAGGCCACGCACTG	600
Db	541	TGAGTCGATATATGGGCTATTGGTTGTGTTTTGCGAGCTCTCTGACAGGCCACGCACTG	600
Qy	601	TGGCCCTGGAAAAATCAGATGTGAACCACTTTATCTGATAATCAGACACTAGGAAAAATTA	660
Db	601	TGGCCCTGGAAAAATCAGATGTGAACCACTTTATCTGATAATCAGACACTAGGAAAAATTA	660
Qy	661	ATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT	720

Db	661	ATCCCAAGACATCAATCAATCTTTAAAGAGTAACGGGTTTTCATGGCATACTATACCT	720
Qy	721	GAGCCAGAGAATCGGAACCTCTTGAGAGAAAGTTCTCAGATGTTTCATCTGTGCTCTG	780
Db	721	GAGCCAGAGAATCGGAACCTCTTGAGAGAAAGTTCTCAGATGTTTCATCTGTGCTCTG	780
Qy	781	AAC TTCATGAAGGGGTGCTCGAAGTGAATCCAGATGACAGATTAACTGTGTTCCCAATC	840
Db	781	AAC TTCATGAAGGGGTGCTCGAAGTGAATCCAGATGACAGATTAACTGTGTTCCCAATC	840
Qy	841	CTGAGAGCTCCTACTTTTGATCTTTTTCAGAGGCCCAAAATTAAGAAAAAGACAGTAAT	900
Db	841	CTGAGAGCTCCTACTTTTGATCTTTTTCAGAGGCCCAAAATTAAGAAAAAGACAGTAAT	900
Qy	901	GAAGGAAGAAACAGAAGACGCCAACAGGTACTTCGGCTCAAAAAGT	945
Db	901	GAAGGAAGAAACAGAAGACGCCAACAGGTACTTCGGCTCAAAAAGT	945

RESULT 2

RESQ1 2
AAD03814
ID AAD03814 standard; cDNA; 972 BP.

AC AAD03814;

DT 19-JUN-2001 (first entry)

Human kinase cDNA #3.

XX
KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder; ss.

OS Homo sapiens.

Key	Location/Qualifiers
CDS	1..972
FT	/tag= a
FT	/product= "Human kinase #3"
FT	/note= "The coding region d
FT	/partial

XX PD 05-APR-2001

XX
PF 27-SEP-2000: 2000WO-US026621.

AA
PR 28-SEP-1999: 99US-0156511P.

AA
PA
(LEXI-) LEXICON GENETICS INC.

PI Donoho G, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;

AA
DR WPI; 2001-266166/27.
DR P-PSDB; AAE00492.

New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.

PS Disclosure; Page 29-30; 38pp; English.

The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays for the identification of other cellular gene

CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ

Sequence 972 BP; 323 A; 172 C; 214 G; 263 T; 0 U; 0 Other;

Query Match 98.3%; Score 929; DB 4; Length 972;
 Best Local Similarity 100.0%; Pred. No. 6.8e-240;
 Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCAAAAGTATGAAAATTAGCTTAAGCTGAGAGGCTCTTATGGGTTGTATTCAAA 60
 Db |||||
 Qy 1 ATGCAAAAGTATGAAAATTAGCTTAAGCTGAGAGGCTCTTATGGGTTGTATTCAAA 60
 Db |||||
 Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTACTGTGTAATAAATTGTGGAACTCTGAAGAT 120
 Db |||||
 Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTACTGTGTAATAAATTGTGGAACTCTGAAGAT 120
 Db |||||
 Qy 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db |||||
 Qy 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db |||||
 Qy 181 CCAATCTGTGACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTAAGTTT 240
 Db |||||
 Qy 181 CCAATCTGTGACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTAAGTTT 240
 Db |||||
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 Db |||||
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 Db |||||
 Qy 301 GGAGTGATCAAAAGCGTATTAATGCAACACTTCAAGCTCTTAATTTCTGTGATATACAT 360
 Db |||||
 Qy 301 GGAGTGATCAAAAGCGTATTAATGCAACACTTCAAGCTCTTAATTTCTGTGATATACAT 360
 Db |||||
 Qy 361 AACTGTATTCACAGATATATAACCTGAAATATTTCTAATTAAGCAAGGAATATC 420
 Db |||||
 Qy 361 AACTGTATTCACAGATATATAACCTGAAATATTTCTAATTAAGCAAGGAATATC 420
 Db |||||
 Qy 421 AAGATTTGTGACTTTCGGTTTGCACAAATCTGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||
 Qy 421 AAGATTTGTGACTTTCGGTTTGCACAAATCTGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||
 Qy 481 GTAGCTACGAGATGTTACCGAGCTCCTGAACTTCTTGTGGAGATACCTAGTATGTTCT 540
 Db |||||
 Qy 481 GTAGCTACGAGATGTTACCGAGCTCCTGAACTTCTTGTGGAGATACCTAGTATGTTCT 540
 Db |||||
 Qy 541 TCAGTCATATATGGCTATGTTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
 Db |||||
 Qy 541 TCAGTCATATATGGCTATGTTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
 Db |||||
 Qy 601 TGGCTCGAAATCAGATGTGGACCACTTTATCTGATATCAAGACACTAGGAAATTA 660
 Db |||||
 Qy 601 TGGCTCGAAATCAGATGTGGACCACTTTATCTGATATCAAGACACTAGGAAATTA 660
 Db |||||
 Qy 661 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 720
 Db |||||
 Qy 661 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 720
 Db |||||
 Qy 721 GAGCCAGACATGGAACCTCTTGGAGAAAGTTCTCAGATGTTCACTGTGGCTCTG 780
 Db |||||
 Qy 721 GAGCCAGACATGGAACCTCTTGGAGAAAGTTCTCAGATGTTCACTGTGGCTCTG 780
 Db |||||
 Qy 781 AACTTCATGAGGGGTCTGTAAGATGAATCCAGATGACGATTAACCTGTTCCCACTC 840
 Db |||||
 Qy 781 AACTTCATGAGGGGTCTGTAAGATGAATCCAGATGACGATTAACCTGTTCCCACTC 840
 Db |||||

Qy 841 CTGAGAGCTCTCTACTTTGATTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGCTAAT 900
 Db |||||
 Qy 841 CTGAGAGCTCTCTACTTTGATTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGCTAAT 900
 Db |||||
 Qy 901 GAACGAGAAACAGACAGACGCCACACAGT 929
 Db |||||
 Qy 901 GAACGAGAAACAGACAGACGCCACACAGT 929
 Db |||||
 RESULT 3
 AAD30557
 ID AAD30557 standard; cDNA; 1790 BP.
 AC AAD30557;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Human kinase polypeptide (PKIN-10) cDNA.
 XX
 KW Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease;
 KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
 KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
 KW cholestasis; candida; cardiovascular disorder; Niemann-Pick's disease;
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
 KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
 KW hypotensive; anti-HIV; enzyme; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 239..1267
 FT /*tag= a
 FT /product= "Human PKIN-10"
 XX
 FN WO200208399-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 20-JUL-2001; 2001WO-US023092.
 XX
 PR 21-JUL-2000; 2000US-0220038P.
 PR 28-JUL-2000; 2000US-022112P.
 PR 04-AUG-2000; 2000US-0222831P.
 PR 11-AUG-2000; 2000US-0224729P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PA (THOR/) THORNTON M.
 XX
 PI Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK,
 PI Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
 PI Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
 PI Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
 PI Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
 XX
 DR WPI; 2002-206083/26.
 DR P-PSDB; AAE19152.
 XX
 FT New human kinase polypeptide, useful in diagnosis, prevention and
 FT treatment of cancer, immune disorder, growth and developmental disorder,
 FT cardiovascular disorder and lipid disorder.
 XX
 PS Claim 5; Page 183; 196pp; English.
 XX
 CC The present invention relates to an isolated human kinase polypeptide
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
 CC useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
 CC bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a

CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 CC drug screening techniques and to analyse the proteome of a tissue or cell
 CC type. PKIN is useful for creating knockin humanised animals or transgenic
 CC animals to model human diseases, in somatic or germline gene therapy, to
 CC generate a transcript image of a tissue or cell type, for detecting
 CC differences in the chromosomal location due to translocation, inversion,
 CC etc., among normal, carrier or affected individuals, and as hybridisation
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful
 CC in southern or northern analysis, dot blot or other membrane-based
 CC technologies, in PCR technologies, in dipstick, pin, microformat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-10 cDNA
 XX
 SQ Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 U; 0 Other;

Query Match 98.1%; Score 927; DB 6; Length 1790;
 Best Local Similarity 100.0%; Pred. No. 3e-239;
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAAGATGATAAAATAGCTAGAGCTGAGAGGGTCTATGGGGTGTATTTCAA 60
 Db 239 ATGGAAAGATGATAAAATAGCTAGAGCTGAGAGGGTCTATGGGGTGTATTTCAA 298
 QY 61 TGAGAAACAAACCTCTGACAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120
 Db 299 TGAGAAACAAACCTCTGACAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 358
 QY 121 GATCTGTTGTTAAGAAATAGCATTAGAGAAATACGTATTTGAAGCAATTTAAACAT 180
 Db 359 GATCTGTTGTTAAGAAATAGCATTAGAGAAATACGTATTTGAAGCAATTTAAACAT 418
 QY 181 CCAATCTTTGTGAACCTCATCGAGTGTTTCAGGAGAAAGAAATGCAATTTAGTTT 240
 Db 419 CCAATCTTTGTGAACCTCATCGAGTGTTTCAGGAGAAAGAAATGCAATTTAGTTT 478
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
 Db 479 GAATCTGTGATCATACACTTTTAAATGAGTGGAAAGAAACCCAAATGGAGTTGCTGAT 538
 QY 301 GGAGTGATCAAAAGCGTATTATGCAAAACCTTCAAGCTCTTAATTTCTGCATATACAT 360
 Db 539 GGAGTGATCAAAAGCGTATTATGCAAAACCTTCAAGCTCTTAATTTCTGCATATACAT 598
 QY 361 AACTGTATTCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC 420
 Db 599 AACTGTATTCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC 658
 QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTGATTCAGAGATGCTTACACCGATTAT 480
 Db 659 AAGATTTGTGACTTCGGGTTTGCACAAATTTGATTCAGAGATGCTTACACCGATTAT 718
 QY 481 GTAGTACGAGATGGTATCCGAGCTTCCTGAATCTTCTGCGAGATACCTAGTATGTTCT 540
 Db 719 GTAGTACGAGATGGTATCCGAGCTTCCTGAATCTTCTGCGAGATACCTAGTATGTTCT 778
 QY 541 TCAGTCCATATATGGGCTATGTTGTTGTTTTCAGAGCTTCCTGACAGCCAGCCACTG 600
 Db 779 TCAGTCCATATATGGGCTATGTTGTTGTTTTCAGAGCTTCCTGACAGCCAGCCACTG 838
 QY 601 TGGCTTGGAAATCAGATGTGGACCACTTTATCTGATATATCAGACACTAGGAAATTA 660
 Db 839 TGGCTTGGAAATCAGATGTGGACCACTTTATCTGATATATCAGACACTAGGAAATTA 998
 QY 661 ATCCCAAGACATCATCATCTTTTAAAGTAAACGGGTTTTTCCATGGCATCATGATACCT 720
 Db 899 ATCCCAAGACATCATCATCTTTTAAAGTAAACGGGTTTTTCCATGGCATCATGATACCT 958
 QY 721 GAGCCAGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTCTATCTGCGCTCTG 780
 Db 959 GAGCCAGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTCTATCTGCGCTCTG 1018

QY 781 AACTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACATTAACCTGTTCCCACTC 840
 Db 1019 AACTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACATTAACCTGTTCCCACTC 1078
 QY 841 CTGAGAGCTCCTACTTTTGTATCTTTTCAAGAGCCCAAAATTTAAAGAAAGACGATTAAT 900
 Db 1079 CTGAGAGCTCCTACTTTTGTATCTTTTCAAGAGCCCAAAATTTAAAGAAAGACGATTAAT 1138
 QY 901 GAAGGAAGAAACACAGACGCGCAACAG 927
 Db 1139 GAAGGAAGAAACACAGACGCGCAACAG 1165

RESULT 4
 ABX08936
 ID ABX08936 standard; cDNA; 1678 BP.
 XX
 AC ABX08936;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE cDNA encoding human DITHP protein #6.
 KW Human; ss; gene; diagnostic and therapeutic; DITHP; cancer;
 KW arteriosclerosis atherosclerosis; psoriasis; primary thrombocytopenia;
 KW autoimmune; inflammatory; anaemia; asthma; autoimmune thyroiditis;
 KW Crohn's disease; diabetes mellitus; glomerulonephritis; gout; stroke;
 KW multiple sclerosis; rheumatoid arthritis; uveitis; AIDS; allergy;
 KW acquired immunodeficiency disease; neurological disorder; epilepsy;
 KW Alzheimer's disease; dementia; mental retardation; gastrointestinal;
 KW Parkinson's disease; ulcer; cirrhosis; reproductive; infertility;
 KW endometriosis; endocrine disorder; hyperparathyroidism; hyperlipidemia;
 KW hypercholesterolemia; hypoglycaemia; obesity; Reiter's syndrome;
 KW connective tissue disorder; osteoporosis; infection.
 XX
 OS Homo sapiens.
 XX
 PN WC200279473-A2.
 XX
 PD 10-OCT-2002.
 XX

PF 09-JAN-2002; 2002WO-US001009.
 XX
 XX 12-JAN-2001; 2001US-0261622P.
 PR 16-JAN-2001; 2001US-0261864P.
 PR 16-JAN-2001; 2001US-0261865P.
 PR 17-JAN-2001; 2001US-0262164P.
 PR 17-JAN-2001; 2001US-0262207P.
 PR 17-JAN-2001; 2001US-0262208P.
 PR 17-JAN-2001; 2001US-0262209P.
 PR 17-JAN-2001; 2001US-0262215P.
 PR 18-JAN-2001; 2001US-0263102P.
 PR 19-JAN-2001; 2001US-0262599P.
 PR 19-JAN-2001; 2001US-0262662P.
 PR 19-JAN-2001; 2001US-0262760P.
 PR 19-JAN-2001; 2001US-0263063P.
 PR 19-JAN-2001; 2001US-0263064P.
 PR 19-JAN-2001; 2001US-0263065P.
 PR 19-JAN-2001; 2001US-0263069P.
 PR 19-JAN-2001; 2001US-0263077P.
 PR 19-JAN-2001; 2001US-0263329P.
 PR 19-JAN-2001; 2001US-0263330P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;
 PI Dam TC, Liu TF, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;
 PI Chang SC, Gerstin EH, Peralta CH, David MH, Lewis SA;
 XX WPI; 2003-040680/03.
 DR P-PSDB; ABU05290.
 XX

PT New human diagnostic and therapeutic (DITHP) polynucleotides and
 PT polypeptides, useful for diagnosing, preventing or treating diseases,
 PT e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory
 PT diseases.
 XX
 XX
 PS Claim 1; Page 267; 331pp; English.
 PS
 XX
 CC This invention relates to the cDNA and protein sequences of fifty six
 CC polynucleotides for diagnostics and therapeutics (DITHP). The human DITHP
 CC polynucleotides and polypeptides are useful for diagnosing, preventing or
 CC treating diseases associated with, as well as effects of exogenous
 CC compounds, on the expression of human molecules, such as cell
 CC proliferative diseases (e.g. cancer, arteriosclerosis atherosclerosis,
 CC psoriasis, primary thrombocytopenia), autoimmune/inflammatory diseases
 CC (e.g. anaphylaxis, asthma, autoimmune thyroiditis, Crohn's disease, diabetes
 CC mellitus, glomerulonephritis, gout, multiple sclerosis, rheumatoid
 CC arthritis, uveitis), acquired immunodeficiency disease; AIDS; allergies;
 CC neurological disorders (e.g. stroke, Alzheimer's disease, dementia,
 CC mental retardation, Parkinson's disease, epilepsy), gastrointestinal
 CC (e.g. ulcer, cirrhosis), reproductive (e.g. infertility, endometriosis),
 CC endocrine disorders (e.g. hyperparathyroidism, hypercholesterolemia,
 CC hypoglycaemia, hyperlipidemia, obesity), connective tissue disorders
 CC (e.g. osteoporosis, Reiter's syndrome), or infections (e.g. bacterial,
 CC viral, fungal, parasitic, protozoal). The DITHP sequences may be used to
 CC generate hybridisation probes useful in chromosomal mapping of naturally
 CC occurring genomic sequences. They are also useful in designing probes
 CC useful in diagnostic assays. The polynucleotides are useful as molecular
 CC weight markers, or as antigen to elicit an immune response. The present
 CC sequence represents a human diagnostics and therapeutics (DITHP) cDNA
 CC sequence of the invention
 XX
 SQ Sequence 1678 BP; 541 A; 308 C; 336 G; 493 T; 0 U; 0 Other;
 Query Match 91.9%; Score 868.8; DB 10; Length 1678;
 Best Local Similarity 99.2%; Pred. No. 1.4e-223;
 Matches 925; Conservative 0; Mismatches 2; Indels 5; Gaps 5;
 Qy 1 ATGGAAGAGTATGAAAATTAGCTAAGACTGAGAGAGGCTTTATGGGTTGATTCAA 60
 Db 131 ATGGAGAGTATGAAAATTAGCTAAGACTGAGAGAGGCTTTATGGGTTGATTCAA 190
 Qy 61 TGCAGA-AACAAAACCTCTGCACAGTAGTAGCTTTAAATAATTTGGGAATCTGAGA 119
 Db 191 TGCAGATTAACAAAACCTCTGCACAGTAGTAGCTTTAAATAATTTGGGAATCTGAGA 250
 Qy 120 TGATCTCTGTTAAGAAAATAGCACTAAGAAATACGTA-TGTTGAAGCAATTAATAAC 178
 Db 251 TGATCTCTGTTAAGAAAATAGCACTAAGAAATACGTA-TGTTGAAGCAATTAATAAC 310
 Qy 179 ATCCAAATCTTGTGAACCTCTATCGAGGTTTTCAGAGAAAAGGAAATATGATTAGTTT 238
 Db 311 ATCCAAATCTTGTGAACCTCTATCGAGGTTTTCAGAGAAAAGGAAATATGATTAGTTT 370
 Qy 239 TTGATATCTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGAGTTCGT 298
 Db 371 TTGATATCTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGAGTTCGT 430
 Qy 299 ATGAGTGCATCAAGAGCGTATTTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATAC 358
 Db 431 ATGAGTGCATCAAGAGCGTATTTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATAC 490
 Qy 359 ATAATCTGATTACAGAGATATAAAACCTGAAAATATTCTTAATACTAAGCAAGGAATAA 418
 Db 491 ATAATCTGATTACAGAGATATAAAACCTGAAAATATTCTTAATACTAAGCAAGGAATAA 550
 Qy 419 TCAAGATTGTGACTTCGGGTTTGCACAAATCTGATTCAGGAGATGCTTACACCGATT 478
 Db 551 TCAAGATTGTGACTTCGGGTTTGCACAAATCTGATTCAGGAGATGCTTACACCGATT 610
 Qy 479 ATGTAGCTA-CGAGATGTCACCGAGCT-CCTGAACTCTTCTGGGAGATCT-CAGTATG 535
 Db 611 ATGTAGCTAGGAGATGTCACCGAGCTCCCTGAACTCTTCTGGGAGATCTCAGTATG 670

Qy 536 GTTCTTCAGTCGATATATGGCTATTGGTTGTTGTTTTCAGAGCTCTCTGACAGCCAGC 595
 Db 671 GTTCTTCAGTCGATATATGGCTATTGGTTGTTGTTTTCAGAGCTCTCTGACAGCCAGC 730
 Qy 596 CACTGTGGCCCTGGAAAATCAGATGTGGACCAACTTTATCTGATATATCAGAACACTAGGAA 655
 Db 731 CACTGTGGCCCTGGAAAATCAGATGTGGACCAACTTTATCTGATATATCAGAACACTAGGAA 790
 Qy 656 AATTAATCCCAAGACATCAATCAATCTTTTAAAGTAAACGGGTTTTCATGGCATCAGTA 715
 Db 791 AATTAATCCCAAGACATCAATCAATCTTTTAAAGTAAACGGGTTTTCATGGCATCAGTA 850
 Qy 716 TACCTGAGCCAGACATCAATCAATCTTTTAAAGTAAACGGGTTTTCATGGCATCAGTA 775
 Db 851 TACCTGAGCCAGACATCAATCAATCTTTTAAAGTAAACGGGTTTTCATGGCATCAGTA 910
 Qy 776 CTCTGAACTTCAATCAATCAATCTTTTAAAGTAAACGGGTTTTCATGGCATCAGTA 835
 Db 911 CTCTGAACTTCAATCAATCAATCTTTTAAAGTAAACGGGTTTTCATGGCATCAGTA 970
 Qy 836 AACTCTGAGAGCTCTCTTACTTTTCAAGAGGCCCAATTAATAAGAAAGAACAC 895
 Db 971 AACTCTGAGAGCTCTCTTACTTTTCAAGAGGCCCAATTAATAAGAAAGAACAC 1030
 Qy 896 GTAATGAGGAGAGAAACAGAGAGCCCAACAG 927
 Db 1031 GTAATGAGGAGAGAAACAGAGAGCCCAACAG 1062
 RESULT 5
 AAS06725
 ID AAS06725 standard; cDNA; 1083 BP.
 XX
 AC AAS06725;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Polynucleotide sequence encoding human protein kinase #25.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200138503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX
 XX WPI; 2001-343950/36.
 DR P-PSDB; AAU03525.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX
 PS Example 1; Fig 1; 433pp; English.
 XX
 CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with

inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.

SQ Sequence 1083 BP; 366 A; 199 C; 225 G; 293 T; 0 U; 0 Other;

Query Match 91.3%; Score 863; DB 4; Length 1083;
Best local alignment: 91.3%; Score 863; DB 4; Length 1083;

Best Local Similarity 94.5%; Pred. NO. 4.3e-222;
Matches 927; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

QY		1	ATGGAAGTATGAAAAATTAGCTAAGACTGGAGAAGGTCTTTATGGGTTGTATTCAA	60
Db		1	ATGGAAGTATGAAAAATTAGCTAAGCTGGAGAAGGTCTTTATGGGTTGTATTCAA	60
QY		61	TCCAGAAACAAAACCTCTGGCAAGTAGTAGTGCTTTAAAAAATTTGTGGAATCTGAAGAT	120
Db		61	TGCAGAAACAAAACCTCTGGCAAGTAGTAGTGCTTTAAAAAATTTGTGGAATCTGAAGAT	120
QY		121	GATCCTCGTTGTTAAGAAAAATAGCACTAAGAGNAATACGTATGTTGAAGCAATTAAACAAT	180
Db		121	GATCCTCGTTGTTAAGAAAAATAGCACTAAGAGNAATACGTATGTTGAAGCAATTAAACAAT	180
QY		181	CCAAATCTTGTGAACCTCATCGAGGTGCTTCAGGAGAAAAAGGAAAAATGCATTTAGTTTTT	240
Db		181	CCAAATCTTGTGAACCTCATCGAGGTGCTTCAGGAGAAAAAGGAAAAATGCATTTAGTTTTT	240
QY		241	GAATACTGTGATCATACACTTTTAATAGACTGGAAAGAAACCCAATGGAGTGTGCTGAT	300
Db		241	GAATACTGTGATCATACACTTTTAATAGACTGGAAAGAAACCCAATGGAGTGTGCTGAT	300
QY		301	GGAGTGAATCAAAACGGTATTATGCGCAACACTTCAAGCTCTTAAATTCGTGCATATACAT	360
Db		301	GGAGTGAATCAAAACGGTATTATGCGCAACACTTCAAGCTCTTAAATTCGTGCATATACAT	360
QY		361	AACCTGTATTACAGAGATAAAAAACCTGAAAAATTTCTAATAACTAAGCAAGGAATAATC	420
Db		361	AACCTGTATTACAGAGATAAAAAACCTGAAAAATTTCTAATAACTAAGCAAGGAATAATC	420
QY		421	AAGATTTGTGACTTCGGGTTGACAAAATCTCGA-----454	
Db		421	AAGATTTGTGACTTCGGGTTGACAAAATCTCGAGTAATTCACATGTTGGGAGAAATTGAC	480
QY		455	-----TTCCAGAGAGATGCCCTAACCGATTTATGTAGCT	486
Db		481	TTACCTGATCTGATTTGANGATTTGCAGTTCAGAGAGATGCCCTAACCGATTTATGTAGCT	540
QY		487	ACGAGATGTPACCGAGCTCCTGAATCTTGTGGGAGATACCTCAGTATGGTCTTCTCAGTC	546
b		541	ACGAGATGTPACCGAGCTCCTGAATCTTGTGGGAGATACCTCAGTATGGTCTTCTCAGTC	600
QY		547	GATATATGGGCTAATGGTTGTGTTTTCAGAGCTCCTGACAGGCCACCGCACTGTGGCCT	606
b		601	GATATATGGGCTAATGGTTGTGTTTTCAGAGCTCCTGACAGGCCACCGCACTGTGGCCT	660
QY		607	GGAAAAATCAGATGTGGACCACCTTTATCTGATTAATCAGAACACTAGGAAAAATTAATCCCC	666
b		661	GGAAAAATCAGATGTGGACCACCTTTATCTGATTAATCAGAACACTAGGAAAAATTAATCCCC	720
QY		667	AGACATCAATCAATCTTTAAAAAGTAAACGGTTTTTCCATGSCATCAGTATACCTGAGCCA	726
b		721	AGACATCAATCAATCTTTAAAAAGTAAACGGTTTTTCCATGSCATCAGTATACCTGAGCCA	780
QY		727	GAAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGTTCTATCCTGTGGCTCTGAACCTTC	786

Claim 5; SEQ ID NO 94; 330pp; English.

The present sequence encodes a human kinase and phosphatase (KPP) protein. KPP sequences have cardiovascular, antiarteriosclerotic, hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic, antiasthmatic, immunosuppressive, antithyroid, dermatological, antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological, antiarheumatic, antiparkinsonian, cytostatic, anticonvulsant, hepatotropic, CNS, antipsoriatic, haemostatic, myotropic, antilipemic, antiparasitic, antihelminthic, antibacterial, virucide, antitubercular, antiparasitic activities, and can be used in gene therapy, and as kinase modulators and phosphatase modulators. KPP proteins, polynucleotides, agonists and antagonists can be used for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, such as cardiovascular diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris or congestive heart failure), immune system disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, dementia or epilepsy), disorders affecting growth and development (e.g. cirrhosis, hepatitis, mixed connective tissue disease, psoriasis or primary thrombocytopenia), cell proliferative disorders (e.g. cancer), hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP and polynucleotides are also useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases, or for facilitating the drug discovery process, including determination of efficacy, dosage, toxicity and pharmacology. The polynucleotides encoding KPP are useful for creating transgenic animals to model human disease.

Sequence 1429 BP; 466 A; 286 C; 294 G; 383 T; 0 U; 0 Other;

Query Match	74.5%;	Score	704.4;	DB	12;	Length	1429;
Best Local Similarity	82.2%;	Pred. No.	2.7e-179;				
Matches	924;	Conservative	0;	Mismatches	1;	Indels	199;
Gaps							

QY	1	ATGGAAAAGTATGAAAATTTAGCTAAGACTGGAGAAGGCTCTTATGGGTTGTATTCAAA	60
Db	70	ATGGAAAAGTATGAAAATTTAGCTAAGACTGGAGAAGGCTCTTATGGGTTGTATTCAAA	129
QY	61	TGCAGAACAAAACCTCTGGACAAGTAGTAGCTGTTTAAAAAATTTTGTGGAATCTGAAGAT	120
Db	130	TGCAGAACAAAACCTCTGGACAAGTAGTAGCTGTTTAAAAAATTTTGTGGAATCTGAAGAT	189
QY	121	GATCCTGTGTTTAGAAAAATAGCACATAAGAGAAATACGTATCTGAAGCAATTTAAAAACAT	180
Db	190	GATCCTGTGTTTAGAAAAATAGCACATAAGAGAAATACGTATCTGAAGCAATTTAAAAACAT	249
QY	181	CCAAATCTTGTGACCTCATCGAGGTGTTTCAGAGAAAAGSAAAATGCAITTTAGTTTTT	240
Db	250	CCAAATCTTGTGAACTCATCGAGGTGTTTCAGAGAAAAGSAAAATGCAITTTAGTTTTT	309
QY	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTGTCTGAT	300
Db	310	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTGTCTGAT	369
QY	301	GGAGTGTATCAAAAAGCGTATTATGGCAACACATTCGAAGCTCTTAATTTCTGTGCATATACAT	360
Db	370	GGAGTGTATCAAAAAGCGTATTATGGCAACACATTCGAAGCTCTTAATTTCTGTGCATATACAT	429
QY	361	AACCTGTATTCACAGAGATATAAACTGGAATATTTCTAATACTAAGCAAGGAATAATC	420
Db	430	AACCTGTATTCACAGAGATATAAACTGGAATATTTCTAATACTAAGCAAGGAATAATC	489
QY	421	AGATTGTGACTTCGGGTTTGCACAAATTTCTG-----	453
Db	490	AGATTGTGACTTCGGGTTTGCACAAATTTCTGAACACAGTGTGTTACCATGGGGCCCAAG	549

FT CDS 129..815
 FT /*tag= b
 FT /product= "Protein kinase 14275"
 FT 816..882
 FT /*tag= c
 XX
 PN WO200179488-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 13-APR-2001; 2001WO-US012188.
 XX
 PR 13-APR-2000; 2000US-0196910P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Kapeller-Libermann R;
 XX
 DR WPI; 2002-034355/04.
 DR P-PSDB; AAG78547.
 XX
 XX New 14257 polypeptides (protein kinases), useful as diagnostic targets
 PT and therapeutic agents for controlling cellular proliferative and/or
 PT differentiative disorder, bone disorders, immune disorders and
 PT cardiovascular disorders.
 XX
 PS Claim 2; Fig 1A; 98pp; English.
 XX
 CC The invention relates to an isolated 14257 polypeptide and nucleic acid
 CC encoding it. The 14257 protein is a protein kinase that acts as a
 CC modulating agent in regulating a variety of cellular processes, including
 CC cell proliferation, differentiation, growth and division. The activity of
 CC the protein of the invention may be described as; cytoskeletal; osteopathic
 CC ; hepatotropic; antidiabetic; neuroprotective; antiarthritic;
 CC dermatological; immunosuppressive; antiinflammatory; antithyroid;
 CC antipsoriatic; ophthalmological; antiallergic; antiasthmatic;
 CC antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide;
 CC anorectic; metabolic; immunomodulator and analgesic. The protein of the
 CC invention may act as a novel diagnostic target or therapeutic agent
 CC controlling certain disorders, for example kinase-associated or other
 CC 14257-associated disorders. These may include cellular proliferative
 CC disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's
 CC disease. Other disorders include bone metabolism disorders such as
 CC osteoporosis, disorders of the immune system, e.g. inflammatory,
 CC diabetes mellitus, osteoarthritis and asthma. Proteins of the invention
 CC may also be of use as therapeutic agents in cardiovascular disorders such
 CC as hypertension and coronary artery disease, and some endothelial cell
 CC disorders, including psoriasis. The current sequence represents a human
 CC kinase 14257 cDNA
 XX
 SQ Sequence 882 BP; 288 A; 150 C; 198 G; 245 T; 0 U; 1 Other;
 Query Match 68.3%; Score 645.4; DB 6; Length 882;
 Best Local Similarity 99.1%; Pred. No. 1.8e-163;
 Matches 649; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ATGGAAAGTATGAAATTAAGCTAAGACTGAGAGGGTCTTATGGGGTTGATTCAAA 60
 DB 129 ATGGGAAGTATGAAATTAAGCTAAGACTGAGAGGGTCTTATGGGGTTGATTCAAA 188
 QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
 DB 189 TGCAGAAACAAACCTCTGGCABAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 248
 QY 121 GATCCTGTGTTAGAAATAGCACTAGAGAAATACGTATGTCAGCAATTAACAT 180
 DB 249 GATCCTATGTTAGAAATAGCACTAGAGAAATACGTATGTCAGCAATTAACAT 308
 QY 181 CCAATCTTGTGAACCTCATCCAGTGTTCAGGAGAAAGAAATGCAATTTAGTTT 240
 DB 309 CCAATCTTGTGAACCTCATCCAGTGTTCAGGAGAAAGAAATGCAATTTAGTTT 368
 QY 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTGTCTGAT 300

Db 369 GAATACTGTGATCATGACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 428
 QY 301 GGAGTGTATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTTGTTCATATACAT 360
 Db 429 GGAGTGTATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTTGTTCATATACAT 488
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
 Db 489 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 548
 QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATCTGATTCAGGAGATGCTACACGATTAT 480
 Db 549 AAGATTTGTGACTTCGGGTTTGCACAAATCTGATTCAGGAGATGCTACACGATTAT 608
 QY 481 GTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATATCTCAGTATGTTCT 540
 Db 609 GTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATATCTCAGTATGTTCT 668
 QY 541 TCAGTGCATATATGGGCTATTGGTTGTTTTTTCAGAGCTCTTCGACAGGCCAGCCACTG 600
 Db 669 TCAGTGCATATATGGGCTATTGGTTGTTTTTTCAGAGCTCTTCGACAGGCCAGCCACTG 728
 QY 601 TGGCCTGAAAATCAGATGTGGACCACTTTATCTGATATCAGAACACTAGGAA 655
 Db 729 TGGCCTGAAAATCAGATGTGGACCACTTTATCTGATATCAGAACACTAGGAA 783
 RESULT 11
 AAF44669
 ID AAF44669 standard; cDNA; 911 BP.
 XX
 AC AAF44669;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase cDNA, SEQ ID NO: 49.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disease; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014842.
 XX
 PR 28-MAY-1999; 99US-0136503P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
 XX
 DR WPI; 2001-032161/04.
 DR P-PSDB; AAB65642.
 XX
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 XX
 PS Example 4; Fig 2; 310pp; English.
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and

complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and disorders include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders

Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;
 Query Match 68.0%; Score 643; DB 4; Length 911;
 Best Local Similarity 100.0%; Pred. No. 7.9e-163;
 Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 285 AATGGAGTTCCTGATGGAGTATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAA 344
 1 AATGGAGTTCCTGATGGAGTATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAA 60
 345 TTCTGTCTATATACATAAATCTGATTCACAGAGATATAAAACCTGAAATTTCTATATAC 404
 61 TTCTGTCTATATACATAAATCTGATTCACAGAGATATAAAACCTGAAATTTCTATATAC 120
 405 TAAGCAAGGAATAATCAAGATTTGTGACTTCGCGTTTGCAAAATTTCTGATTCAGGAGA 464
 121 TAAGCAAGGAATAATCAAGATTTGTGACTTCGCGTTTGCAAAATTTCTGATTCAGGAGA 180
 465 TGCTTACACCGATTTATGTAGTACGAGATGTTACCGAGTCTCTGAACTTTTGTGGGAGA 524
 181 TGCTTACACCGATTTATGTAGTACGAGATGTTACCGAGTCTCTGAACTTTTGTGGGAGA 240
 525 TACTCAGTATGTTCTTCACTGATATATGCGCTATTTGTTGTTTTCAGAGCTCCT 584
 241 TACTCAGTATGTTCTTCACTGATATATGCGCTATTTGTTGTTTTCAGAGCTCCT 300
 585 GACAGCCAGCCACTGTGCGCTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 644
 301 GACAGCCAGCCACTGTGCGCTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 360
 645 AACCTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTTTTCCTCA 704
 361 AACCTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTTTTCCTCA 420
 705 TGGCATCAGTATACCTGAGCCAGACAGATCGAACTCTTGAGAAAGTTCTCAGATGT 764
 421 TGGCATCAGTATACCTGAGCCAGACAGATCGAACTCTTGAGAAAGTTCTCAGATGT 480
 765 TCATCCTGTGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 824
 481 TCATCCTGTGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 540
 825 AACCTGTCCCAACTCTCGAGAGCTCCTACTTTGATTTCTTTTCAAGAGCCCAATTTAA 884
 541 AACCTGTTCCTCAACTCTCGAGAGCTCCTACTTTGATTTCTTTTCAAGAGCCCAATTTAA 600
 885 AAGAAAAGCAGTAATGAAGGAAGAAACAGACGCGCCACAG 927
 601 AAGAAAAGCAGTAATGAAGGAAGAAACAGACGCGCCACAG 643

RESULT 12
 ADI29367
 ID ADI29367 standard; cDNA; 911 BP.
 XX
 AC ADI29367;
 AC
 DT 22-APR-2004 (first entry)
 XX
 DE Human MARK3-associated cDNA #37.

XX
 KW Human; ss; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003232771-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 17-JUN-2002; 2002US-00174319.
 XX
 PR 17-JUN-2002; 2002US-00174319.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ward DT, Freier SM, Dobie KW;
 XX
 DR WPI; 2004-052188/05.
 DR P-PSDB; ADI29249.
 XX
 New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX
 Disclosure; Fig 2; 233pp; English.
 XX
 The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated cDNA included in the figures but not mentioned anywhere else in the specification.
 XX
 SQ Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;

Query Match 68.0%; Score 643; DB 12; Length 911;
 Best Local Similarity 100.0%; Pred. No. 7.9e-163;
 Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 285 AATGGAGTTCCTGATGGAGTATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAA 344
 Db 1 AATGGAGTTCCTGATGGAGTATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAA 60
 QY 345 TTCTGTCTATATACATAAATCTGATTCACAGAGATATAAAACCTGAAATTTCTATATAC 404
 Db 61 TTCTGTCTATATACATAAATCTGATTCACAGAGATATAAAACCTGAAATTTCTATATAC 120
 QY 405 TAAGCAAGGAATAATCAAGATTTGTGACTTCGCGTTTGCAAAATTTCTGATTCAGGAGA 464
 Db 121 TAAGCAAGGAATAATCAAGATTTGTGACTTCGCGTTTGCAAAATTTCTGATTCAGGAGA 180
 QY 465 TGCTTACACCGATTTATGTAGTACGAGATGTTACCGAGTCTCTGAACTTTTGTGGGAGA 524
 Db 181 TGCTTACACCGATTTATGTAGTACGAGATGTTACCGAGTCTCTGAACTTTTGTGGGAGA 240
 QY 525 TACTCAGTATGTTCTTCACTGATATATGCGCTATTTGTTGTTTTCAGAGCTCCT 584
 Db 241 TACTCAGTATGTTCTTCACTGATATATGCGCTATTTGTTGTTTTCAGAGCTCCT 300
 QY 585 GACAGCCAGCCACTGTGCGCTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 644
 Db 301 GACAGCCAGCCACTGTGCGCTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 360

Qy 645 AACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA 704
 Dd |||||
 Qy 361 AACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA 420
 Dd |||||
 Qy 705 TGGCATCAGTATACCTGAGCCAGAGACATCGAACTCTTGAGGAAAGTTCTCAGATGT 764
 Dd |||||
 Qy 421 TGGCATCAGTATACCTGAGCCAGAGACATCGAACTCTTGAGGAAAGTTCTCAGATGT 480
 Dd |||||
 Qy 765 TCATCTGTGGCTCTGAACTTTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 824
 Dd |||||
 Qy 481 TCATCTGTGGCTCTGAACTTTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 540
 Dd |||||
 Qy 825 AACCTGTTCCCACTCTCGAGAGCTCTACTTTGATTTCTTTCAAGAGGCCCAATTA 884
 Dd |||||
 Qy 541 AACCTGTTCCCACTCTCGAGAGCTCTACTTTGATTTCTTTCAAGAGGCCCAATTA 600
 Dd |||||
 Qy 885 AAGAAAGACGTAATGAAGGAAGAAACAGAGAGCGCCAAACAG 927
 Dd |||||
 Qy 601 AAGAAAGACGTAATGAAGGAAGAAACAGAGAGCGCCAAACAG 643
 Dd |||||

RESULT 13
 AAF44670
 ID AAF44670 standard; cDNA; 2615 BP.
 XX
 AC AAF44670;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase cDNA, SEQ ID NO: 50.
 XX

Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 immunosuppressive; cardiac; renal; antiinflammatory; antiaesthetic;
 dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 immune disorder; cardiovascular disease; neurodegenerative disease;
 cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 Mus musculus.

W0200073469-A2.
 XX
 XX
 PD 07-DEC-2000.
 XX
 XX 26-MAY-2000; 2000WO-US014842.
 XX
 XX 28-MAY-1999; 99US-0136503P.
 XX
 XX (SUGG-) SUGEN INC.
 XX
 XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
 XX
 XX WPI; 2001-032161/04.
 XX
 XX P-PSDB; AAB65643.

Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 treating immune-related diseases and disorders, cardiovascular disease,
 neurodegenerative diseases and/or cancers.

Disclosure; Fig 2; 310pp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune

CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 CC stress related disorders, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
 CC disorders
 XX
 SQ Sequence 2615 BP; 742 A; 580 C; 585 G; 708 T; 0 U; 0 Other;

Query Match 59.2%; Score 559.2; DB 4; Length 2615;
 Best Local Similarity 81.8%; Pred. No. 4.6e-140;
 Matches 658; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

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 Qy 58 CCTCATCGAGGTGTTGAGGAGAAAGAAAGATGATCTAGTTTTCGATCTGATCA 117
 Dd |||||
 Qy 255 TACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAG 314
 Dd |||||
 Qy 118 CACACTGTTAAACGAGCTGGAGAGAACCCAAACGGAGTTTCTGATGGAGTATTAAG 177
 Dd |||||
 Qy 315 CGTATTATGGCAAACTTCAAGCTCTTAATTTCTGTCATATACATTAATCTGTATTCAG 374
 Dd |||||
 Qy 178 TGTGCTATGGCAAACTTCAAGCTCTTAATTTCTGTCATATACATTAATCTGTATTCAG 237
 Dd |||||
 Qy 375 AGATATAAAACCTGAAATATTTCTAATACTAGCAGGAGTAATCAAGTTTCTGACTT 434
 Dd |||||
 Qy 238 GGAATATAAAACCTGAAATATTTCTAATACTAGCAGGAGTAATCAAGTTTCTGACTT 297
 Dd |||||
 Qy 435 CGGTTTGGCAAACTTCTGATTCAGGAGATGCTTACACCGATTATCTAGCTAGCAGATG 494
 Dd |||||
 Qy 298 TGAATTTGACGATTTCTAATTCAGGAGAGCTTACACAGACTATGTTGCCACAGGTG 357
 Dd |||||
 Qy 495 GTACCGAGCTCTGAACTTTCTGTTGGAGATACCTAGTATGTTTCTGATGATATATG 554
 Dd |||||
 Qy 358 GTACCGAGCTCTGAACTTTCTGTTGGAGAGACAGGAGTACGTTCTCTGTAGACGTG 417
 Dd |||||
 Qy 555 GGTATTTGTTGTTGTTTTCAGAGCTCTGAGAGCGCCAGCTGTTGGCTGGAAATC 614
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 Qy 418 GCGCGTGGCTGTTGTTTTCAGAGCTCTGAGAGCGGTGAGCCACTTGGCGGGAATC 477
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 Qy 598 GGAAGCTCTTTGAAAGAAATTTCTCAATGTTTACGCTGTTGCTTAAAGTTTCATGAGGG 657
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 Qy 795 GTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGCTCTTA 854
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 Qy 658 ATGCTGAAGATGAATCCTGATGAGGCTGACCTGTGCCAGCTGTGACAGCTGCTTA 717
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 Qy 855 CTTTGTATCTTTTCAAGAGGCCCAATTAATAAGAAAGACGTAATCAAGAGGAGAAACAG 914
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RESULT 14
 ADI29368
 ID ADI29368 standard; cDNA; 2615 BP.

XX ADI29368;
AC 22-APR-2004 (first entry)
XX Mouse MARK3-associated cDNA #12.
XX Mouse; ss; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.
XX Mus musculus.
XX US2003232771-A1.
XX 18-DEC-2003.
XX 17-JUN-2002; 2002US-00174319.
XX 17-JUN-2002; 2002US-00174319.
XX (ISIS-) ISIS PHARM INC.
XX Ward DT, Freier SM, Dobie KW;
XX WPI; 2004-052188/05.
XX P-PSDB; ADI29250.
XX New antisense compound targeted to a nucleic acid molecule encoding
XX microtubule-affinity-regulating kinases (MARK3), useful for modulating
XX expression of MARK3 or for treating cancer or Alzheimer's disease.
XX Disclosure; Fig 2; 233pp; English.
XX The invention relates to a compound comprising a sequence comprising 8-80
XX base pairs (bp) targeted to a nucleic acid encoding MARK3
XX (MAP/microtubule affinity-regulating kinase 3), that specifically
XX hybridizes with the nucleic acid encoding MARK3 and inhibits expression
XX of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
XX composition comprising the compound and a carrier or diluent, inhibiting
XX the expression of MARK3 in cells or tissues, treating an animal having or
XX suspected of having a disease or condition associated with MARK3 and
XX screening for an antisense compound. The antisense oligonucleotide is
XX useful for preparing a composition for treating hyperproliferative
XX disorder, particularly cancer and neurodegenerative diseases e.g.
XX Alzheimer's disease. The present sequence is a MARK3 associated cDNA
XX included in the figures but not mentioned anywhere else in the
XX specification.
XX Sequence 2615 BP; 742 A; 580 C; 585 G; 708 T; 0 U; 0 Other;
Query Match 59.2%; Score 559.2; DB 12; Length 2615;
Best Local Similarity 81.8%; Pred. No. 4.6e-140;
Matches 658; Conservative 0; Mismatches 143; Indels 3; Gaps 1;
QY 135 GAAATAGCACTAAGAGAAATACGTATGTTCAAGCAATTAATAATCAATCTCTGAA 194
Db 1 GAAATAGCCCTGCGGAAATCGTATGTAAG--TTGAACACCCAACTCGTAA 57
QY 195 CCTCATCGAGTGTTCAGAGAAAGAAATGCAATTTAGTTTGAATCTGTGATCA 254
Db 58 CCTCATCGAGTGTTCAGAGAAAGAAATGCAATTTAGTTTGAATCTGTGATCA 117
QY 255 TACACTTTTAAATGAGCTGGAAGAAACCCAAATCGAGTTGCTGATGAGTCAATCAAG 314
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QY 555 GGCTATTGTTGTTGTTTTCAGAGCTCTCTGACAGGCGACGACCTGTTGGCTCGAAATC 614
Db 418 GCGCTGCGCTGTGTTTTCAGAGCTCTCTGACGCGGTACGCCACTCTGGCCGGGAAATC 477
QY 615 AGATGTGACCACTTTTCTGATATATCAAGAACATAGGAAATTAATCCAAAGACATCA 674
Db 478 CGAGCTGGACCACTTTTCTGATATATCAAGAACATAGGAAATTAATCCAAAGACATCA 537
QY 675 ATCAATCTTTAAAGTAACGGGTTTTTCCATGTCATCAGTATATACCTGAGCCAGACAT 734
Db 538 GTCTATCTTTAGGAGTAACCCAGTTTTTTCGCGGCATCAGCATACCTGAAACAGACAT 597
QY 735 GGAACCTCTTTCAGGAAAGTTTCTCAGATGTTTCACTGTTGCTGCTGAACTTCATGAAGG 794
Db 598 GGAGACTCTTTGAAAGAAATTTCTCAATGTTTCAAGCTGTGGCTTTAAAGTTTCATGAAGG 657
QY 795 GTGCTGAGATCAATCCAGATGACAGATTAACTGTTTCCCACTCTCCAGCTCTGAGAGCTCTA 854
Db 658 ATGCTTGAAGATGAACTCTGATGAGAGGCTGACCTGTGCTCCAGCTGTGAGCAGTGCTTA 717
QY 855 CTTTGTATCTTTTCAAGAGGCCCAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAG 914
Db 718 CTTTGTAGTCTTTTCAAGAGGATCAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAG 914
QY 915 AAGACGCCCAACAGTACTTTCGCT 938
Db 778 AAGGCCCAACAGTACTTTCGCT 801
RESULT 15
ABX34679
ID ABX34679 standard; cDNA; 1281 BP.
XX ABX34679;
XX AC
XX 13-FEB-2003 (first entry)
XX DE Human mddt cDNA SEQ ID 240.
XX MDDT; human; disease detection and treatment molecule polypeptide;
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW gene therapy; protein replacement therapy; cell proliferative disorder;
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; sarcoma;
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
KW psoriasis; hepatitis; gene; ss.
OS Homo sapiens.
XX WO200279449-A2.
XX 10-OCT-2002.
XX 27-MAR-2002; 2002WO-US009944.
XX 28-MAR-2001; 2001US-0279619P.
XX 29-MAR-2001; 2001US-0280667P.
XX 29-MAR-2001; 2001US-0280668P.
XX 16-MAY-2001; 2001US-0291280P.
XX 17-MAY-2001; 2001US-0291829P.
XX 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleeefeld Y, Gerstein EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RV, Urashka ME;
 XX WPI; 2003-058431/05.
 DR P-PSDB; ABU11689.
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 PS Claim 1; SEQ ID NO 240; 339pp + Sequence Listing; English.
 XX
 CC This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDPT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABX34440-ABX34835 encode the MDPT polypeptides represented in
 CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1281 BP; 428 A; 191 C; 317 G; 345 T; 0 U; 0 Other;
 Query Match 57.5%; Score 543.2; DB 8; Length 1281;
 Best Local Similarity 99.5%; Pred. No. 7.1e-136;
 Matches 545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATGCAAAAGTATGAAAAATTAGCTAAGACTGAGAGGGCTTATGGGTTGTATTCAAA 60
 DB 704 ATGAAAAGTATGAAAAATTAGCTAAGACTGAGAGGGCTTATGGGTTGTATTCAAA 763
 QY 61 TGCAGAAACAAACCTCTGGACAAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 DB 764 TGCAGAAACAAACCTCTGGACAAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 823
 QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAAAACAT 180
 DB 824 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAAAACAT 883
 QY 181 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGGAGAAAAGGAAAATGCAATTTAGTTT 240
 DB 884 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGGAGAAAAGGAAAATGCAATTTAGTTT 943
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 DB 944 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 1003
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 DB 1184 GCAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTCAGTATGGTTCT 1243
 QY 541 TCAGTCGA 548
 DB 1244 TCAGTCAA 1251

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-766-691-11
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Scoring table: IDENTITY NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

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Listing first 45 summaries

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12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	945	100.0	945	6	AX107722 Sequence
3	929	98.3	972	6	AR492167 Sequence
4	929	98.3	972	6	AX107716 Sequence
5	927	98.1	1790	6	AX746179 Sequence
6	868.8	91.9	1678	6	AX698820 Sequence
7	863	91.3	1083	6	AX166534 Sequence
8	839	88.8	1041	6	AR492169 Sequence
9	839	88.8	1041	6	AX107720 Sequence
10	823	87.1	1068	6	AR492166 Sequence
11	823	87.1	1068	6	AX107714 Sequence
12	647	68.5	687	6	AX286069 Sequence
13	647	68.5	882	6	AX286067 Sequence
14	643	68.0	911	6	AX056404 Sequence
15	559.2	59.2	2615	6	AX056405 Sequence
16	507	53.7	1819	6	AR492171 Sequence
17	507	53.7	1819	6	AX107724 Sequence
18	501	53.0	1086	6	AX803417 Sequence
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21	454.4	48.1	594	6	AR492168
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23	451.4	47.8	1525	5	BC079506
24	416.4	44.1	1861	10	BC081896
25	415.4	44.0	1612	6	AX399975
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27	413.8	43.8	2944	6	CQ492706
28	400.2	42.3	2952	3	AK112442
29	360.8	38.2	538	6	CQ714922
30	287	30.4	1701	6	AR221995
31	287	30.4	1701	6	AR438689
32	287	30.4	3080	6	AR221994
33	287	30.4	3080	6	AR438688
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35	283.8	30.0	1993	9	HSU35146
36	280.6	29.7	1061	5	CR407462
37	275.8	29.2	2132	10	BC083590
38	274	29.0	1179	6	CQ588387
39	272.6	28.8	1518	10	AB029067
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ALIGNMENTS

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VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
ORIGIN

AR492170
Sequence 11 from patent US 6716616.
AR492170
AR492170.1 GI:47260680
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Unclassified.
1 (bases 1 to 945)
Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
Human kinase proteins and polynucleotides encoding the same
Patent: US 6716616-A 11 06-APR-2004;
Location/Qualifiers
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Query Match 100.0%; Score 945; DB 6; Length 945;

Best Local Similarity 100.0%; Pred. No. 1.7e-205;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
AR492167
LOCUS
DEFINITION
ACCESSION
AR492167
Sequence 5 from patent US 6716616.
DNA linear PAT 15-MAY-2004

VERSION AR492167.1 GI:47260677
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 972)
AUTHORS Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 5 06-APR-2004;
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Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX107716 972 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0123579.
ACCESSION AX107716
VERSION AX107716.1 GI:13923199
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 5 05-APR-2001;
Lexicon Genetics Incorporated (US)
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Query Match 98.3%; Score 929; DB 6; Length 972;
Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 30 from Patent WO0208399.
 ACCESSION AX746179
 VERSION AX746179.1 GI:31746165

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
 AUTHORS Yue, H., Khan, F.A., Gururajan, R., Hafalia, A.J., Chawla, N.K.,
 Arvizu, C.S., Ramkumar, J., Gandhi, A.R., Policky, J.L., Baughn, M.R.,
 Tribouley, C.M., Bandman, O., Nguyen, D.B., Lu, Y., Burford, N., Lal, P.,
 Ding, L., Yao, M.G., Elliott, V.S., Recipon, S.A., Kearney, L., Lu, D.A.,
 Greenwald, S.R., Tang, Y.T., Xu, Y., Walsh, R.T., Gietzen, K.J.,
 Yang, J., Jackson, J.L. and Thornton, M.
 Human kinases
 TITLE Patent: WO 0208399-A 30 31-JAN-2002;
 JOURNAL Incyte Genomics, Inc. (US); Thornton, Michael (US)
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 Best Local Similarity 100.0%; Pred. No. 2e-201;
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RESULT 6
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 LOCUS AX698820 1678 bp DNA linear PAT 02-APR-2003
 DEFINITION Sequence 6 from Patent WO02079473.
 ACCESSION AX698820
 VERSION AX698820.1 GI:29499608
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 AUTHORS Panzer, S.R., Lincoln, S.E., Altus, C.M., Dufour, G.E., Hillman, J.L.,
 Jones, A.L., Dam, T.C., Liu, T.F., Harris, B., Flores, V., Daffo, A.,
 Marwaha, R., Chen, A.J., Chang, S.C., Gerstin, J.E., Peralta, C.H.,
 David, M.H. and Lewis, S.A.


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DEFINITION Sequence 9 from patent US 6716616.
ACCESSION AR492169
VERSION    AR492169.1  GI:47260679
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1041)
AUTHORS    Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
            and Sands,A.T.
TITLE      Human kinase proteins and polynucleotides encoding the same
JOURNAL    Patent: US 6716616-A 9 06-APR-2004;
FEATURES   Location/Qualifiers
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Query Match      88.8%; Score 839; DB 6; Length 1041;
Best Local Similarity 90.8%; Pred. No. 2.8e-181;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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LOCUS      1041 bp          DNA          linear          PAT 30-APR-2001
DEFINITION Sequence 9 from Patent WO0123579.
ACCESSION AX107720
VERSION    AX107720.1  GI:13923201
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowicz,B. and Sands,A.T.
AUTHORS    Human kinase proteins and polynucleotides encoding the same
TITLE      Patent: WO 0123579-A 9 05-APR-2001;
JOURNAL    Lexicon Genetics Incorporated (US)

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Query Match      88.8%; Score 839; DB 6; Length 1041;
Best Local Similarity 90.8%; Pred. No. 2.8e-181;
Matches 945; Conservative 0; Mismatches 96; Gaps 1;

Qy 1 ATGGAAGATGATAAAATAGCTTAAGACTGAGAGGGCTTATGGGTTGTATTCAAA 60
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DEFINITION   Sequence 3 from patent US 6716616.
ACCESSION   AR492166
VERSION      AR492166.1   GI:47260676
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 1068)
AUTHORS      Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
              and Sands,A.T.
TITLE        Human kinase proteins and polynucleotides encoding the same
JOURNAL      Patent: US 6716616-A 3 06-APR-2004;
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 DEFINITION Sequence 3 from Patent WO0123579.
 ACCESSION AX107714
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 ORGANISM Homo sapiens
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 1 Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.
 Human kinase proteins and polynucleotides encoding the same
 JOURNAL Patent: WO 0123579-A 3 05-APR-2001;
 Lexicon Genetics Incorporated (US)
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 VERSION AX286069.1 GI:17045995
 KEYWORDS
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 ORGANISM Homo sapiens
 DNA 687 bp
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AUTHORS Kapeller-Libermann, R.
TITLE 14257, protein kinase molecules and uses therefor
JOURNAL Patent: WO 0179488-A 3 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
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ACCESSION AX286067
VERSION AX286067.1 GI:17045993
KEYWORDS Homo sapiens (human)
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REFERENCE 1
AUTHORS Kapeller-Libermann, R.
TITLE 14257, protein kinase molecules and uses therefor
JOURNAL Patent: WO 0179488-A 1 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 99.2%; Pred. No. 2.2e-137;
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LOCUS
DEFINITION
AX056404
SEQUENCE 48 from Patent WO0073469.
ACCESSION
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VERSION
AX056404.1 GI:12229111
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
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AUTHORS
Plowman, G.D., Martinez, R., Whyte, D. and Sudersanam, S.
TITLE
Protein kinases
JOURNAL
Patent: WO 0073469-A 48 07-DEC-2000;
Sugen, Inc. (US)
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REFERENCE
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AUTHORS
Plowman, G.D., Martinez, R., Whyte, D. and Sudersanam, S.
TITLE
Protein kinases
JOURNAL
Patent: WO 0073469-A 49 07-DEC-2000;
Sugen, Inc. (US)
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GenCore version 5.1.6
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Minimum DB seq length: 0
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4	1636	98.4	347	4 AAE00494	Aae00494 Human kin
5	1619	97.4	360	4 AAU03525	Aau03525 Human pro
6	1612	97.0	356	4 AAE00491	Aae00491 Human kin
7	1296.5	78.0	296	4 AAB65643	Aab65643 Novel pro
8	1296.5	78.0	296	8 ADI29250	ADI29250 Mouse MAR
9	1188.5	71.5	358	5 ABP62954	Abp62954 Human pro
10	1183.5	71.2	358	8 ADO01538	Ado01538 Human cyc
11	1149	69.1	247	4 AAB65642	Aab65642 Novel pro
12	1149	69.1	247	8 ADI29249	ADI29249 Human MAR
13	1140	68.6	228	5 AAG78547	Ag78547 Human kin
14	1027.5	61.8	392	4 ABB63118	Abb63118 Drosophil
15	967.5	58.2	566	3 AAY90724	Aay90724 Rabbit KK
16	948	57.0	197	6 ABU11689	Abu11689 Human MDD
17	941.5	56.6	493	7 ADC77659	Adc77659 Human 162
18	941.5	56.6	493	8 ADQ89156	Adq89156 Human uro
19	937.5	56.4	362	6 ABP96087	Abp96087 Human pro
20	791	47.6	183	8 ADI40875	Adi40875 Human kin
21	791	47.6	187	4 AAE00490	Aae00490 Human kin
22	791	47.6	198	4 AAE00493	Aae00493 Human kin
23	791	47.6	205	8 ADK71868	Adk71868 Human kin
24	784.5	47.2	455	3 AAY70126	Aay70126 Human los
25	784.5	47.2	455	8 ADI57233	Adi57233 NKIAMRE d

26	784.5	47.2	455	8 ADI57214	Adi57214 Human NKI
27	784.5	47.2	455	8 ADI57236	Adi57236 CDK3 domi
28	784.5	47.2	591	4 AAU03524	Aau03524 Human pro
29	763.5	45.9	457	3 AAY70125	Aay70125 Rat lost
30	763.5	45.9	505	3 AAY70124	Aay70124 Rat lost
31	725	43.6	562	8 ABM83922	Abm83922 Human dia
32	712.5	42.9	154	6 ABU05290	Abu05290 Human dia
33	656	39.5	534	4 AAB65645	Aab65645 Novel pro
34	656	39.5	534	8 ADI29252	ADI29252 Human MAR
35	581	35.0	305	7 ADP45039	Adp45039 Human kin
36	581	35.0	305	7 ADJ68738	Adj68738 Human hea
37	581	35.0	305	8 ADI57200	Adi57200 Human CDK
38	581	35.0	305	8 ADI57237	Adi57237 CDK3 domi
39	581	35.0	333	4 AAM39276	Aam39276 Human pol
40	574	34.5	352	4 AAM41062	Aam41062 Human pol
41	570	34.3	298	2 AAW95689	Aaw95689 Homo sapi
42	570	34.3	544	2 AAW85028	Aaw85028 CDK2-gree
43	570	34.3	544	2 AAW85029	Aaw85029 Green flu
44	569	34.2	224	4 ABG06142	Abg06142 Novel hum
45	569	34.2	298	7 ADD21390	Add21390 Human cyc

ALIGNMENTS

RESULT 1
AAE00495
ID AAE00495 standard; protein; 315 AA.

XX AAE00495;
AC AAE00495;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human kinase #6.
XX
KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW Biological disorder.
XX
OS Homo sapiens.
XX
PN WO200123579-A1.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026621.
XX
PR 28-SEP-1999; 99US-0156511P.
XX
(LEXI-) LEXICON GENETICS INC.
XX
Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
Sands AT;
XX
WPI; 2001-266166/27.
N-PSDB; AAD03817.

XX
New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
XX
Claim 3; Page 33-34; 38pp; English.
XX
The present sequence is novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinases for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical

disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bio-reactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 315 AA;

Query Match	100.0%;	Score 1662;	DB 4;	Length 315;
Best Local Similarity	100.0%;	Pred. No. 1.5e-168;		
Matches 315;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MEKYEKLAKTGEGSGVGVFKCRNKTSGQVAVVKFVESEDDPVVKKIALRETRMLKQLKH	60	
Db	1	MEKYEKLAKTGEGSGVGVFKCRNKTSGQVAVVKFVESEDDPVVKKIALRETRMLKQLKH	60	
QY	61	PNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI	120	
Db	61	PNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI	120	
QY	121	NCIHRDIKPENILITKOGIITKIDFGPAQILIPGDAYTDVATRWYRAPELLVGDQYGS	180	
Db	121	NCIHRDIKPENILITKOGIITKIDFGPAQILIPGDAYTDVATRWYRAPELLVGDQYGS	180	
QY	181	SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHQSIIFKSNFGFFHGISIP	240	
Db	181	SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHQSIIFKSNFGFFHGISIP	240	
QY	241	EPEDMETLEEKFSVDVHPVALNFMKGCLKNMPDDRLLTCSOLLESSYFDSFQEAQIRRKARN	300	
Db	241	EPEDMETLEEKFSVDVHPVALNFMKGCLKNMPDDRLLTCSOLLESSYFDSFQEAQIRRKARN	300	
QY	301	EGRNRRRQOVLPLKS	315	
Db	301	EGRNRRRQOVLPLKS	315	

RESULT 2

AAE19152

AAE19152:

DT 21-MAY-2002 (first entry)

Human kinase polypeptide (PKIN-10).

Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; burstis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cystostatic; cancer; cholestasis; cardiac; cardiovascular disease; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic; hypotensive; anti-HIV; enzyme.

Homo sapiens.

	Key	Location/Qualifiers
FH	Domain	4. .286
FT		

/note= "Eukaryotic protein kinase domain"

WO200208399-A2.

31-JAN-2002.

20-JUL-2001: 2001WO-US023092-

5

21-JUL-2000; 2000US-0220038P.
28-JUL-2000; 2000US-0222112P.
04-AUG-2000; 2000US-0222831P.
11-AUG-2000; 2000US-0224729P.

(INCY-) INCYTE GENOMICS INC.
(THOR/) THORNTON M.

Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK, Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR; Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L, Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR, Tang YT, Xu Y, Walsh RF, Gietzen KJ, Yang J, Hillman JL;

WPI; 2002-206083/26.
N-PSDE; AAD30557.

Claim 1; Page 147-148; 196pp; English.

The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency disease, AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g., bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful in southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present invention is human PKIN-10.

Sequence 342 AA:

Query Match 98.6%: Score 1639: DB 5: Length 342:

[illegible]

Db 301 EGRNRQQQLLPL 315
RESULT 3
AAE00492
ID AAE00492 standard; protein; 324 AA.
XX AAE00492;
AC AAE00492;
XX 19-JUN-2001 (first entry)
DT Human kinase #3.
DE Human; kinase; gene therapy; bioreactor; mental disorder;
XX biological disorder.
KW Homo sapiens.
XX
XX WO200123579-A1.
XX
XX 05-APR-2001.
XX 27-SEP-2000; 2000WO-US026621.
XX 28-SEP-1999; 99US-0156511P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-266166/27.
XX N-PSDB; AAD03814.
XX
XX New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
XX Disclosure; Page 30; 38pp; English.
XX
XX The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical
CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
CC probes are useful for screening human genomic library for identifying
CC polymorphisms and as primers in amplification assays to detect mutations
CC within the exons, introns and splice sites that can be used in
CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
CC bioreactors in the body delivering a continuous supply of NHP to the
CC body. Nucleotide constructs encoding functional NHPs are used in gene
CC therapy for the modulation of NHP expression
XX
SQ Sequence 324 AA;
Query Match 98.6%; Score 1638; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 5.8e-166; Mismatches 0; Gaps 0;
Matches 310; Conservative 0; Indels 0;
Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRPNVGADVGIKSVLWQTLQALNFCIH 120

Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRPNVGADVGIKSVLWQTLQALNFCIH 120
Qy 121 NCIHRIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLITGOPLWPGKSDVDQLYLIIRTIGLKLIPRHQSIFKSNFGFHGISIP 240
Db 181 SVDIWAIGCVFAELLITGOPLWPGKSDVDQLYLIIRTIGLKLIPRHQSIFKSNFGFHGISIP 240
Qy 241 EPEDMETLEKFSVDHPVVALNFMKGLKMPDDRLTCSQLLESYFDSFQEAQIKRKARN 300
Db 241 EPEDMETLEKFSVDHPVVALNFMKGLKMPDDRLTCSQLLESYFDSFQEAQIKRKARN 300
Qy 301 EGRNRQQQV 310
Db 301 EGRNRQQQV 310
RESULT 4
AAE00494
ID AAE00494 standard; protein; 347 AA.
XX AAE00494;
XX 19-JUN-2001 (first entry)
DT Human kinase #5.
DE Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
XX Homo sapiens.
XX WO200123579-A1.
XX 05-APR-2001.
XX 27-SEP-2000; 2000WO-US026621.
XX 28-SEP-1999; 99US-0156511P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-266166/27.
XX N-PSDB; AAD03816.
XX
XX New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
XX Claim 2; Page 32-33; 38pp; English.
XX
XX The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical
CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
CC probes are useful for screening human genomic library for identifying
CC polymorphisms and as primers in amplification assays to detect mutations
CC within the exons, introns and splice sites that can be used in
CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP

CC products are used to genetically engineer cells in vivo that functions as
CC bioreactors in the body delivering a continuous supply of NHP to the
CC body. Nucleotide constructs encoding functional NHPs are used in gene
CC therapy for the modulation of NHP expression
XX
SQ Sequence 347 AA;

Query Match 98.4%; Score 1636; DB 4; Length 347;
Best Local Similarity 90.8%; Pred. No. 1e-165; Mismatches 0; Indels 32; Gaps 1;
Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKKRKHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCHIH 120
DB 61 PNLVNLIEVFRKKRKHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCHIH 120
QY 121 NCIRDKIPENILITKQGIKICDFGFAQILIPGDATDYVATWYRAPELLVGDTOYGS 180
DB 121 NCIRDKIPENILITKQGIKICDFGFAQILIPGDATDYVATWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTL----- 217
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 218 -----GKLI PRHQSIFKSNFGFHGISIPEPEMETLEEKSDVHPVALNFMKGLK 268
DB 241 VASQSAGITGKLI PRHQSIFKSNFGFHGISIPEPEMETLEEKSDVHPVALNFMKGLK 300
QY 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQQVLPKS 315
DB 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQQVLPKS 347

RESULT 5
AAU03525
ID AAU03525 standard; protein; 360 AA.
XX
AC AAU03525;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human protein kinase #25.
XX
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder.

XX Homo sapiens.
OS
XX WO200138503-A2.
FN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-US032085.
XX
XX 24-NOV-1999; 99US-0167482P.
XX
XX (SUGEN-) SUGEN INC.
PA
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
PI
XX WPI; 2001-343950/36.
DR
DR N-PSDB; AAS06725.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.
XX

PS Claim 7; Fig 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX

SQ Sequence 360 AA;

Query Match 97.4%; Score 1619; DB 4; Length 360;
Best Local Similarity 93.4%; Pred. No. 7.3e-164; Mismatches 0; Indels 20; Gaps 2;
Matches 311; Conservative 2; Mismatches 0; Indels 20; Gaps 2;
QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKKRKHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCHIH 120
DB 61 PNLVNLIEVFRKKRKHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCHIH 120
QY 121 NCIRDKIPENILITKQGIKICDFGFAQIL-----IPGDATDYVA 162
DB 121 NCIRDKIPENILITKQGIKICDFGFAQILNSHVRIDLPDIDAFVPGDAYDYVA 180
QY 163 TRWYRAPELLVGDTOYGSVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTLKGLIP 222
DB 181 TRWYRAPELLVGDTOYGSVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTLKGLIP 240
QY 223 RHQSIFKSNFGFHGISIPEPEMETLEEKSDVHPVALNFMKGLKMNPDRLTCSQLLE 282
DB 241 RHQSIFKSNFGFHGISIPEPEMETLEEKSDVHPVALNFMKGLKMNPDRLTCSQLLE 300
QY 283 SSYFDSFQEAQIKRKARNEGRRRRQ--QVLP 313
DB 301 SSYFDSFQEAQIKRKARNEGRRRRQQNOLLPL 333

RESULT 6
AAE00491
ID AAE00491 standard; protein; 356 AA.

XX
AC AAE00491;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human kinase #2.
XX
KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
OS
XX Homo sapiens.
XX
XX WO200123579-A1.
FN
XX 05-APR-2001.
PD
XX 27-SEP-2000; 2000WO-US026621.
PF
XX 28-SEP-1999; 99US-0156511P.
PR

XX PA (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI: 2001-266166/27.
XX N-PSDB; AAD03813.
XX New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
XX Disclosure; Page 28-29; 38pp; English.
XX
XX The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical
CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
CC probes are useful for screening human genomic library for identifying
CC polymorphisms and as primers in amplification assays to detect mutations
CC within the exons, introns and splice sites that can be used in
CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
CC products are used to genetically engineer cells in vivo that functions as
CC bioreactors in the body delivering a continuous supply of NHP to the
CC body. Nucleotide constructs encoding functional NHPs are used in gene
CC therapy for the modulation of NHP expression
XX
SQ Sequence 356 AA;

Query Match 97.0%; Score 1612; DB 4; Length 356;
Best Local Similarity 90.6%; Pred. No. 4e-163;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
QY 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
DB 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRKMLHVPFYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCFHH 120
DB 61 PNLVNLIEVFRKRKMLHVPFYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCFHH 120
QY 121 NCIRHDIKPENILITKQGIKICDFGFAQLIPGDAYTDVYATRWYRAPELLVGDYQGS 180
DB 121 NCIRHDIKPENILITKQGIKICDFGFAQLIPGDAYTDVYATRWYRAPELLVGDYQGS 180
QY 181 SVDIWAIGCVPAELLTQGPLWPKSDVDOLYLIIRTL----- 217
DB 181 SVDIWAIGCVPAELLTQGPLWPKSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 218 -----GKLI PRHOSIFKSNGFHGISIPEDMETLEEKFSVHPVALNFMKGLK 268
DB 241 VASOSAGITGKLI PRHOSIFKSNGFHGISIPEDMETLEEKFSVHPVALNFMKGLK 300
QY 269 MNPDRILTCQSOLLESSYFDSFQEAQIKRKARNEGRRRRQV 310
DB 301 MNPDRILTCQSOLLESSYFDSFQEAQIKRKARNEGRRRRQV 342

RESULT 7
AAB65643
ID AAB65643 standard; protein; 296 AA.
XX
AC AAB65643;
XX

DT 27-MAR-2001 (first entry)
DE Novel protein kinase, SEQ ID NO: 170.
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX inflammatory pelvic disease; multiple sclerosis; psoriasis.
OS Mus musculus.
XX WO2000073469-A2.
XX 07-DEC-2000.
XX 26-MAY-2000; 2000WO-US014842.
XX 28-MAY-1999; 99US-0136503P.
XX (SUGE-) SUGEN INC.
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX WPI: 2001-032161/04.
DR N-PSDB; AAF44670.
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX Claim 10; Fig 1; 310pp; English.
XX The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 296 AA;
Query Match 78.0%; Score 1296.5; DB 4; Length 296;
Best Local Similarity 50.0%; Pred. No. 1.7e-129;
Matches 243; Conservative 19; Mismatches 5; Indels 3; Gaps 2;
QY 46 KIALREIRMLKOLKHNLNLIIEVFRKRKMLHVPFYCDHTLLNELRPNPGVADGVKIS 105
DB 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKMLHVPFYCDHTLLNELRPNPGVADGVKIS 59
QY 106 VLWQTLQALNFCFHHNCIRHDIKPENILITKQGIKICDFGFAQLIPGDAYTDVYATRW 165
DB 60 VLWQTLQALNFCFHHNCIRHDIKPENILITKQGIKICDFGFAQLIPGDAYTDVYATRW 119
QY 166 YRAPELLVGDYQGSVDIWAIGCVPAELLTQGPLWPKSDVDOLYLIIRTLGKLI PRHQ 225
DB 120 YRAPELLVGDYQGSVDVWAVGCVFAELLTQGPLWPKSDVDOLYLIIRTLGKLI PRHQ 179
QY 226 SIPKSNGFHGISIPEDMETLEEKFSVHPVALNFMKGLKMPDRILTCQSOLLESSY 285
DB 180 SIPRNOFFRGISIPEDMETLEEKFSVHPVALNFMKGLKMPDRILTCQALLDSAY 239

```
QY 286 FDSFQEAQIKRKARNEGRNRQ--QVLPL 313
DB 240 FESFQEDQMKRKARSEGRSRQQLLPL 269

RESULT 8
ID ADI29250
AC ADI29250;
XX ADI29250 standard; protein; 296 AA.
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse MARK3-associated protein #12.
XX
KW Mouse; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.
XX
OS Mus musculus.
XX
XX US2003232771-A1.
XX
XX 18-DEC-2003.
XX
XX 17-JUN-2002; 2002US-00174319.
XX
XX 17-JUN-2002; 2002US-00174319.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Ward DT, Freiler SM, Dobie KW;
XX
XX WPI; 2004-052188/05.
XX
XX N-PSDB; ADI29368.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX microtubule-affinity-regulating kinases (MARK3), useful for modulating
XX expression of MARK3 or for treating cancer or Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 170; 233pp; English.
XX
XX The invention relates to a compound comprising a sequence comprising 8-80
XX base pairs (bp) targeted to a nucleic acid encoding MARK3
XX (MAP/microtubule affinity-regulating kinase 3), that specifically
XX hybridizes with the nucleic acid encoding MARK3 and inhibits expression
XX of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
XX composition comprising the compound and a carrier or diluent, inhibiting
XX the expression of MARK3 in cells or tissues, treating an animal having or
XX suspected of having a disease or condition associated with MARK3 and
XX screening for an antisense compound. The antisense oligonucleotide is
XX useful for preparing a composition for treating hyperproliferative
XX disorder, particularly cancer and neurodegenerative diseases e.g.
XX Alzheimer's disease. The present sequence is a MARK3 associated protein
XX included in the figures but not mentioned anywhere else in the
XX specification.
XX
XX Sequence 296 AA;

Query Match 78.0%; Score 1296.5; DB 8; Length 296;
Best Local Similarity 90.0%; Pred. No. 1.7e-129;
Matches 243; Conservative 19; Mismatches 5; Indels 3; Gaps 2;

QY 46 KIALREIRMLKQLKHPNLVNLIEVFRKRKRWHLVFEYCDHTLNELRNPNGVADGVKIS 105
DB 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKRWHLVFEYCDHTLNELRNPNGVADGVKIS 59
QY 106 VLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQIIPGDYDAYVATRW 165
DB 60 VLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQIIPGDYDAYVATRW 119

us-10-766-691-12.rag 166 YRABELLVGDTQYGSVDIWAIGCVFAELLTGQPLWFGKSDVDQLYLIIRTLGKLI PRHQ 225
120 YRABELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWFGKSDVDQLYLIIRTLGKLI PRHQ 179
226 SIFKSNGFHFGISIPEDMETLEEKSDVHPVALNFWKGLKKNPDRILTCQSOLLESSY 285
180 SIFRSNQFFRGISIPEDMETLEEKFSNVQFVALSMKGLKKNPDRILTCQQLDSAY 239
286 FDSFQEAQIKRKARNEGRNRQ--QVLPL 313
240 FESFQEDQMKRKARSEGRSRQQLLPL 269

RESULT 9
ABP62954
ID ABP62954 standard; protein; 358 AA.
XX
AC ABP62954;
XX
DT 14-OCT-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 391.
XX
XX Human; vulnary; dermatological; neuroprotective; nootropic; cancer;
XX antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
XX antidiabetic; anti-allergic; gene therapy; wound healing; tissue repair;
XX burn; central nervous system disorder; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; immune disorder;
XX autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
XX Homo sapiens.
XX
XX WO200218424-A2.
XX
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US027093.
XX
XX 01-SEP-2000; 2000US-00654935.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
XX WPI; 2002-583321/62.
XX N-PSDB; ABQ93433.
XX
XX New polynucleotide and polypeptides, useful for treatment and diagnosis
XX of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
XX sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
XX sclerosis, diabetes and allergies.
XX
XX Claim 20; SEQ ID NO 391; 284pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising one of
XX 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
XX administering to a mammalian subject a composition comprising the protein
XX (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
XX (I), (II) and (III) are useful for diagnosis and (II) can be used for
XX therapeutic treatment. Diseases that may be treated include wound healing
XX and tissue repair, burns, central nervous system disorders (e.g.
XX Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
XX sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
XX sclerosis, diabetes and allergies. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 358 AA;

Query Match 71.5%; Score 1188.5; DB 5; Length 358;
```


Best Local Similarity 70.5%; Pred. No. 8e-118;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAKKFLSEDDPVVKIATLREIRMLKQLKH 61
Qy 61 PNLVNLLEVFRRKRRLHLVFEYCDHTLLNELRNPNVGVADGVKSVLWQTLQALNFCIH 120
Db 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHLDYRQGVPEHLVKSITWQTLQAVNFCCHK 121
Qy 121 NCIHRIKIPENILITKQIIKICDPGPAQILI-PGDAYTDYVATRWYRAPPELLVGDTOYG 179
Db 122 NCIHRIKIPENILITKHSVVKLCDFGARLLTGSDYITDVARWYRSPPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLGKLI PRHQSIKSNQFFHGISI 239
Db 182 PPVDVWAIGCVFABLLSGVPLWPKGSDVDQYLIIRTKLIGDLIPRHOVFTSNQYFSGVKI 241
Qy 240 PEPDMETLEKFSVDHPVAFNFMKGLKMPDRLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PDPEDMEPLEKFPNISYPALGKLGCLHMDPTERTLTCQELLHHPYFENIREIEDLAKH 301
Qy 300 NE 301
Db 302 NK 303

RESULT 10
AD001538
ID AD001538 standard; protein; 358 AA.
AC AD001538;
XX
XX
XX
XX 29-JUL-2004 (first entry)
XX
XX Human cyclin-dependent kinase like 1 (CDKL1) protein SEQ ID NO:4.

human; cyclin-dependent kinase like 1; CDKL1; branching morphogenesis;
branching morphogenesis modulator; angiogenic disorder;
apoptotic disorder; proliferation disorder; chromosome 14.
XX Homo sapiens.
XX WO2004038372-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033483.
XX
XX 23-OCT-2002; 2002US-0420554P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Plowman GD, Karim PD, Swimmer C, Habeck HA, Koblizek TI;
PI Schulte-Merker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
PI Odenthal JH, Scheel JK, Will TT, Jin Y, Hai B;
XX
XX WPI: 2004-365563/34.
XX N-PSDB; ADO01535.

Use of cyclin-dependent kinase like 1 polypeptides or nucleic acids for
modulating branching morphogenesis in a mammalian cell or for diagnosing
a disease e.g. angiogenic, apoptotic or proliferation disorder in a
patient.
XX
XX Example; SEQ ID NO 4; 52pp; English.
XX
XX The present invention describes the use of a cyclin-dependent kinase like
1 (CDKL1) polypeptide or nucleic acid for modulating branching
morphogenesis in a mammalian cell or for diagnosing a disease in a
patient. Also described: (1) identifying a candidate branching
morphogenesis modulating agent; (2) modulating branching morphogenesis in

CC a mammalian cell comprising contacting the cell with an agent that
specifically binds a CDKL1 polypeptide or nucleic acid; and (3) a method
for diagnosing a disease in a patient. The CDKL1 polypeptide or nucleic
acid is useful for modulating branching morphogenesis in a mammalian
cell. It is also useful for diagnosing a disease, e.g. angiogenic,
apoptotic or proliferation disorder in a patient. The present sequence
represents human CDKL1, which is used in the exemplification of the
present invention. The human CDKL1 gene is located on chromosome 14, more
specifically to 14q22.1.

XX
SQ Sequence 358 AA;
Query Match 71.2%; Score 1183.5; DB 8; Length 358;
Best Local Similarity 71.8%; Pred. No. 2.8e-117;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAKKFLSEDDPVVKIATLREIRMLKQLKH 61
Qy 61 PNLVNLLEVFRRKRRLHLVFEYCDHTLLNELRNPNVGVADGVKSVLWQTLQALNFCIH 120
Db 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHLDYRQGVPEHLVKSITWQTLQAVNFCCHK 121
Qy 121 NCIHRIKIPENILITKQIIKICDPGPAQILI-PGDAYTDYVATRWYRAPPELLVGDTOYG 179
Db 122 NCIHRIKIPENILITKHSVVKLCDFGARLLTGSDYITDVARWYRSPPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLGKLI PRHQSIKSNQFFHGISI 239
Db 182 PPVDVWAIGCVFABLLSGVPLWPKGSDVDQYLIIRTKLIGDLIPRHOVFTSNQYFSGVKI 241
Qy 240 PEPDMETLEKFSVDHPVAFNFMKGLKMPDRLTCSQLLESSYFDSFQEAQ 293
Db 242 PDPEDMEPLEKFPNISYPALGKLGCLHMDPTERTLTCQELLHHPYFENIREIE 295

RESULT 11
AAB65642
ID AAB65642 standard; protein; 247 AA.
AC AAB65642;
XX
XX 27-MAR-2001 (first entry)
XX
XX Novel protein kinase, SEQ ID NO: 169.
XX
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
XX immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
XX dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
XX immune disorder; cardiovascular disease; neurodegenerative disease;
XX cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
XX Homo sapiens.
XX
XX WO2000073469-A2.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US014842.
XX
XX 28-MAY-1999; 99US-0136503P.
XX
XX (SUGE-) SUGEN INC.
XX
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
XX WPI: 2001-032161/04.
XX N-PSDB; AAF44669.
XX
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,

neurodegenerative diseases and/or cancers.

Claim 10; Fig 1; 310pp; English.

The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression, such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders

Sequence 247 AA;

Query Match 69.1%; Score 1149; DB 4; Length 247;
Best Local Similarity 98.6%; Pred. No. 7.7e-114;
Matches 217; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 96 NGVADGVKSVLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 155
DB 1 NGVADGVKSVLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 60
QY 156 AYTDVATRWYRAPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 215
DB 61 AYTDVATRWYRAPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 120
QY 216 TLGKLIPIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKMNPDRL 275
DB 121 TLGKLIPIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKMNPDRL 180
QY 276 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLPL 313
DB 181 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLPL 220

RESULT 12

AD129249
ID AD129249 standard; protein; 247 AA.

AC AD129249;

DT 22-APR-2004 (first entry)

DE Human MARK3-associated protein #37.

KW Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.

OS Homo sapiens.

PN US2003232771-A1.

PD 18-DEC-2003.

XX 17-JUN-2002; 2002US-00174319.

XX 17-JUN-2002; 2002US-00174319.

XX (ISIS-) ISIS PHARM INC.

XX Ward DT, Freier SM, Dobie KW;

XX

DR WPI; 2004-052188/05.

DR N-PSDB; ADI29367.

XX New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.

PS Disclosure; SEQ ID NO 169; 233pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein specification.

XX Sequence 247 AA;

Query Match 69.1%; Score 1149; DB 8; Length 247;
Best Local Similarity 98.6%; Pred. No. 7.7e-114;
Matches 217; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 96 NGVADGVKSVLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 155
DB 1 NGVADGVKSVLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 60
QY 156 AYTDVATRWYRAPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 215
DB 61 AYTDVATRWYRAPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 120
QY 216 TLGKLIPIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKMNPDRL 275
DB 121 TLGKLIPIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKMNPDRL 180
QY 276 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLPL 313
DB 181 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLPL 220

RESULT 13

AAG78547

ID AAG78547 standard; protein; 228 AA.

AC AAG78547;

DT 08-MAR-2002 (first entry)

DE Human kinase 14257 amino acid sequence.

KW Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;
KW antidiabetic; neuroprotective; antiarthritic; dermatological;
KW immunosuppressive; antiinflammatory; antihypertensive; antipsoriatic;
KW ophthalmologic; antiallergic; antiasthmatic; antiatherosclerotic;
KW hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic;
KW immunomodulator; analgesic; cellular proliferative disorder; cancer;
KW acute lymphoblastic leukaemia; Hodgkin's disease;
KW bone metabolism disorder; osteoporosis; immune system disorder;
KW inflammatory disorder; diabetes mellitus; osteoarthritis; asthma;
KW cardiovascular disorder; hypertension; coronary artery disease;
KW endothelial cell disorder; psoriasis.

OS Homo sapiens.

XX Key Location/Qualifiers

PH

FT Domain 4. .218
 FT /note= "eukaryotic protein kinase domain"
 FT Modified-site 9. .15
 FT /note= "tyrosine kinase phosphorylation site"
 FT Modified-site 23. .26
 FT /note= "N-glycosylation site"
 FT Modified-site 27. .32
 FT /note= "N-myristoylation site"
 FT Modified-site 38. .41
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 97. .102
 FT /note= "N-myristoylation site"
 FT Modified-site 132. .134
 FT /note= "serine/threonine protein kinase active-site
 FT signal site"
 FT 161. .218
 FT /note= "kinase transferase protein serine/threonine-
 FT protein ATP-binding II phosphorylation casein alpha chain
 FT domain"
 FT Modified-site 180. .183
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 188. .193
 FT /note= "N-myristoylation site"
 FT Modified-site 204. .211
 FT /note= "tyrosine kinase phosphorylation site"
 FT Modified-site 205. .208
 FT /note= "casein kinase II phosphorylation site"
 FT XX
 PN WO200179488-A2.
 XX
 XX 25-OCT-2001.
 XX
 XX 13-APR-2001; 2001WO-US012188.
 XX
 XX 13-APR-2000; 2000US-0196910P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Kapeller-Libermann R;
 XX
 XX WPI; 2002-034355/04.
 DR N-PSDB; AAI64248.
 DR
 XX
 XX New 14257 polypeptides (protein kinases), useful as diagnostic targets
 PT and therapeutic agents for controlling cellular proliferative and/or
 PT differentiative disorder, bone disorders, immune disorders and
 PT cardiovascular disorders.
 XX
 XX Claim 1c; Fig 1a; 98pp; English.
 PS
 XX
 CC The invention relates to an isolated 14257 polypeptide and nucleic acid
 CC encoding it. The 14257 protein is a protein kinase that acts as a
 CC modulating agent in regulating a variety of cellular processes, including
 CC cell proliferation, differentiation, growth and division. The activity of
 CC the protein of the invention may be described as: cytostatic; osteopathic
 CC ; hepatotropic; antidiabetic; neuroprotective; antiarthritic;
 CC dermatological; immunosuppressive; antiinflammatory; antithyroid;
 CC antipsoriatic; ophthalmological; antiallergic; antiaesthmic;
 CC antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide;
 CC anorectic; metabolic; immunomodulator and analgesic. The protein of the
 CC invention may act as a novel diagnostic target or therapeutic agent
 CC controlling certain disorders, for example kinase-associated or other
 CC 14257-associated disorders. These may include cellular proliferative
 CC disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's
 CC disease. Other disorders include bone metabolism disorders such as
 CC osteoporosis, disorders of the immune system, e.g. inflammatory,
 CC diabetes mellitus, osteoarthritis and asthma. Proteins of the invention
 CC may also be of use as therapeutic agents in cardiovascular disorders such
 CC as hypertension and coronary artery disease, and some endothelial cell
 CC disorders, including psoriasis. The current sequence represents a human
 CC kinase 14257 amino acid sequence
 XX
 SQ Sequence 228 AA;

Query Match 68.6%; Score 1140; DB 5; Length 228;
 Best Local Similarity 98.2%; Pred. No. 6.3e-113;
 Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MEYKEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKTALREIRMLKOLKH 60
 Db 1 MGKYEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPIVKKTALREIRMLKOLKH 60
 Qy 61 PNLVNLIEVFRRRKRMHLVFEYCDHTLLNELERNPNPGVADGVIKSVLWQTLQALNFCHIH 120
 Db 61 PNLVNLIEVFRRRKRMHLVFEYCDHALLNELERNPNPGVADGVIKSVLWQTLQALNFCHIH 120
 Qy 121 NCIHRDKPENILITKQGIKICDFGPAQILIPGDATYDVATRYWYRAPELLVGDTOYGS 180
 Db 121 NCIHRDVKPENILITKQGIKICDFGPAQILIPGDATYDVATRYWYRAPELLVGDTOYGS 180
 Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTIG 218
 Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTIG 218
 RESULT 14
 ABB63118
 ID ABB63118 standard; protein; 392 AA.
 XX ABB63118;
 XX AC
 XX 26-MAR-2002 (first entry)
 XX
 XX Drosophila melanogaster polypeptide SEQ ID NO 16146.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX Drosophila melanogaster.
 OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009231.
 XX
 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL07221.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX Disclosure; SEQ ID NO 16146; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (AB857737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 392 AA;

Query Match 61.8%; Score 1027.5; DB 4; Length 392;

Best Local Similarity 58.4%; Pred. No. 1.5e-100;
Matches 184; Conservative 65; Mismatches 61; Indels 5; Gaps 2;

QY 1 MEKYEKLAKTGECSYGVVFKCRNKTSGOVAVKVFESDDPVPVKIALREIRMLKOLKH 60
DB 1 MDYKELSLGSGSYGVVFKCRNKTSGOVAVKVFESDDPVPVKIALREIRMLKOLKH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120

QY 121 NCIHRIKPENILITKQGIKI CDGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180
DB 121 GCHRIKPENILITKQGIKI CDGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180

QY 181 SVDIWAIGCVFAELTQPLWPKSDVDOLYLIIRTLGLKIPRHOSIFKSNQFPHGISIP 240
DB 181 PVDWAIIGCVFAELTQPLWPKSDVDOLYLIIRTLGLKIPRHOSIFKSNQFPHGISIP 240

QY 241 EPEDMETLEEF--SDVHPVALNFMKGLKXNPPDRITCSQLLESSYFDSF--QEAQIK 295
DB 241 VPPTLEEDKMPAKSQQNPLTIDFLKCKLDKPTKWSCEKLTGHSYFDDYIAKQRELE 300

QY 296 RKARNEGRNRROQV 310
DB 301 HVNSLEAANLRQQOL 315

RESULT 15
AAV90724
ID AAV90724 standard; protein; 566 AA.
XX AAV90724;
DT 15-AUG-2000 (first entry)
DE Rabbit KKIAMRE kinase SEQ ID NO:4.
XX Rabbit; KKIAMRE kinase; learning-induced kinase; learning; memory;
KW cdc2-related kinase; brain; gene therapy; genetic disorder; detection;
XX identification.
OS Oryctolagus cuniculus.
XX WO200020567-A2.
XX 13-APR-2000.
XX 01-OCT-1999; 99WO-US023010.
XX 02-OCT-1998; 98US-0102906P.
XX (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX Thompson RF, Gomi H, Sun W;
XX WPI; 2000-328932/28.
XX N-PSDE; AAA29745.
XX Novel learning induced kinase polynucleotides and polypeptides, useful
PT for the analysis of learning and memory, and for gene therapy.
XX Claim 1; Fig 4; 64pp; English.

The present sequence represents a learning-induced kinase, designated KKIAMRE kinase, which is isolated from rabbit brain tissue. KKIAMRE kinase is a cdc2-related kinase. The KKIAMRE kinase polynucleotides can be used to express recombinant protein for analysis, characterisation or therapeutic use, as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, as chromosome markers or tags, to compare endogenous DNA sequences in patients to identify potential genetic disorders, as probes to hybridise and discover novel related sequences, as a source of PCR primers, and as

an antigen to induce anti-DNA antibodies. The polypeptides can be used in assay to discover biological activity, to raise antibodies, as tissue markers, and to isolate correlative receptors or ligands. The polynucleotides may also be used for gene therapy for the treatment of disorders which are mediated by KKIAMRE kinase

Sequence 566 AA;
Query Match 58.2%; Score 967.5; DB 3; Length 566;
Best Local Similarity 54.6%; Pred. No. 6.9e-94;
Matches 177; Conservative 67; Mismatches 65; Indels 15; Gaps 5;

QY 1 MEKYEKLAKTGECSYGVVFKCRNKTSGOVAVKVFESDDPVPVKIALREIRMLKOLKH 60
DB 1 MEKYEKLAKTGECSYGVVFKCRNKTSGOVAVKVFESDDPVPVKIALREIRMLKOLKH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120

QY 121 NCIHRIKPENILITKQGIKI CDGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 179
DB 121 NCIHRIKPENILITKQGIKI CDGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180

QY 180 SVDIWAIGCVFAELTQPLWPKSDVDOLYLIIRTLGLKIPRHOSIFKSNQFPHGISI 239
DB 180 SVDIWAIGCVFAELTQPLWPKSDVDOLYLIIRTLGLKIPRHOSIFKSNQFPHGISI 240

QY 240 PEPEMETLEEFSDVHPVALNFMKGLKXNPPDRITCSQLLESSYF--DSF-----QEA 292
DB 240 PEPEMETLEEFSDVHPVALNFMKGLKXNPPDRITCSQLLESSYF--DSF-----QEA 292

QY 293 QIK--RKARN-----EGRNRROQ 309
DB 301 QMKVQKDARNISLSKKSQNRKKEK 324

Search completed: April 22, 2005, 06:47:32
Job time : 88.5529 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2005, 04:37:19 ; Search time 30.929 Seconds
(without alignments)
760.272 Million cell updates/sec

Title: US-10-766-691-12

Perfect score: 1662

Sequence: 1 MEKYEKLAKTGEYSYGVVFK.....RKARNEGRNRROQVLPLKS 315

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCJTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1662	100.0	315	4	US-09-671-050-12	Sequence 12, Appl
2	1638	98.6	324	4	US-09-671-050-6	Sequence 6, Appl
3	1636	98.4	347	4	US-09-671-050-10	Sequence 10, Appl
4	1612	97.0	356	4	US-09-671-050-4	Sequence 4, Appl
5	1188.5	71.5	367	4	US-09-949-016-7552	Sequence 7552, Ap
6	1183.5	71.2	358	4	US-09-411-628-11	Sequence 11, Appl
7	1183.5	71.2	358	4	US-10-174-794-11	Sequence 11, Appl
8	967.5	58.2	566	4	US-09-411-628-4	Sequence 4, Appl
9	967.5	58.2	566	4	US-10-174-794-4	Sequence 4, Appl
10	941.5	56.6	475	4	US-09-949-016-7954	Sequence 7954, Ap
11	941.5	56.6	493	4	US-09-411-628-10	Sequence 10, Appl
12	941.5	56.6	493	4	US-10-174-794-10	Sequence 10, Appl
13	791	47.6	187	4	US-09-671-050-2	Sequence 2, Appl
14	791	47.6	198	4	US-09-671-050-8	Sequence 8, Appl
15	581	35.0	305	4	US-09-538-092-1236	Sequence 1236, Ap
16	581	35.0	305	4	US-09-949-016-6052	Sequence 6052, Ap
17	581	35.0	334	4	US-09-949-016-10777	Sequence 10777, A
18	570	34.3	298	2	US-08-874-347-25	Sequence 25, Appl
19	570	34.3	298	2	US-08-969-106-2	Sequence 2, Appl
20	570	34.3	298	3	US-09-093-522-25	Sequence 25, Appl
21	570	34.3	298	4	US-09-338-125-2	Sequence 2, Appl
22	570	34.3	298	4	US-09-266-225D-14	Sequence 14, Appl
23	570	34.3	544	4	US-09-417-197-113	Sequence 113, App
24	570	34.3	544	4	US-09-417-197-115	Sequence 115, App
25	569	34.2	298	4	US-09-411-628-13	Sequence 13, Appl
26	569	34.2	298	4	US-10-174-794-13	Sequence 13, Appl
27	568.5	34.2	294	2	US-08-874-347-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1:

US-09-671-050-12

; Sequence 12, Application US/09671050

; Patent No. 6716616

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and

; FILE REFERENCE: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0046-USA

; CURRENT APPLICATION NUMBER: US/09/671.050

; CURRENT FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: US 60/156,511

; PRIOR FILING DATE: 1999-09-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 315

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-671-050-12

Query Match 100.0%; Score 1662; DB 4; Length 315;

Best Local Similarity 100.0%; Pred. No. 1.1e-166;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALRIRMLKQLKH 60

Db 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALRIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKKMHLVFEYCDHTLLNELRPNGVADGVIKSLVWQLQALNFCIH 120

Db 61 PNLVNLIEVFRKKMHLVFEYCDHTLLNELRPNGVADGVIKSLVWQLQALNFCIH 120

Qy 121 NCIRHDIKPNILITKQGIKICDFGFAQLIPGDAYTDDYVATRYRAPELLVGDTOYGS 180

Db 121 NCIRHDIKPNILITKQGIKICDFGFAQLIPGDAYTDDYVATRYRAPELLVGDTOYGS 180

Qy 181 SVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLGKLIPIRHSQIFKSNGFHGISIP 240

Db 181 SVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLGKLIPIRHSQIFKSNGFHGISIP 240

Qy 241 EPDMETLEKFSVDHPVAFNMKGCLMKMPDRLTCSQLLESSYFDSFQEAQIKRKARN 300

Db 241 EPDMETLEKFSVDHPVAFNMKGCLMKMPDRLTCSQLLESSYFDSFQEAQIKRKARN 300

28 568.5 34.2 294 3 US-09-093-522-26 Sequence 26, Appl
29 567 34.1 298 3 US-09-457-040B-29 Sequence 29, Appl
30 567 34.1 298 4 US-09-538-092-1006 Sequence 1006, Ap
31 567 34.1 354 4 US-09-949-016-8025 Sequence 8025, Ap
32 565 34.0 297 1 US-08-176-620A-16 Sequence 16, Appl
33 565 34.0 297 2 US-08-461-985-16 Sequence 16, Appl
34 557 33.5 297 2 US-08-874-347-23 Sequence 23, Appl
35 557 33.5 297 3 US-09-093-522-23 Sequence 23, Appl
36 556 33.5 297 2 US-08-874-347-24 Sequence 24, Appl
37 556 33.5 297 3 US-09-093-522-24 Sequence 24, Appl
38 556 33.5 297 4 US-09-411-628-12 Sequence 12, Appl
39 556 33.5 297 4 US-10-174-794-12 Sequence 12, Appl
40 555.5 33.4 300 2 US-08-874-347-10 Sequence 10, Appl
41 555.5 33.4 300 3 US-09-093-522-10 Sequence 10, Appl
42 555 33.4 270 2 US-07-857-224B-31 Sequence 31, Appl
43 551 33.2 274 1 US-08-318-947A-20 Sequence 20, Appl
44 551 33.2 274 2 US-08-795-303-20 Sequence 20, Appl
45 551 33.2 299 4 US-09-949-016-10673 Sequence 10673, A

Qy 301 EGRNRERQVLPKLS 315
 Db 301 EGRNRERQVLPKLS 315

RESULT 2

US-09-671-050-6
 ; Sequence 6, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-6

Query Match 98.6%; Score 1638; DB 4; Length 324;
 Best Local Similarity 100.0%; Pred. No. 3.8e-164;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
 Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
 Qy 61 PNLVNLIEVFRFRKRKMHVFEYCDHTLLNELRNPNVGADGVKSVLWOTLOALNFCIH 120
 Db 61 PNLVNLIEVFRFRKRKMHVFEYCDHTLLNELRNPNVGADGVKSVLWOTLOALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Db 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Qy 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELTSSDPPA 240
 Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELTSSDPPA 240
 Qy 241 EPEDMETLEEKFSVHPVFNFMKGLKMPDRLTCSQLLESSYFDSFOEAQIKRKARN 300
 Db 241 EPEDMETLEEKFSVHPVFNFMKGLKMPDRLTCSQLLESSYFDSFOEAQIKRKARN 300
 Qy 301 EGRNRERQV 310
 Db 301 EGRNRERQV 310

RESULT 3

US-09-671-050-10
 ; Sequence 10, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA

FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 347
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-10

Query Match 98.4%; Score 1636; DB 4; Length 347;
 Best Local Similarity 90.8%; Pred. No. 6.9e-164;
 Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
 Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
 Qy 61 PNLVNLIEVFRFRKRKMHVFEYCDHTLLNELRNPNVGADGVKSVLWOTLOALNFCIH 120
 Db 61 PNLVNLIEVFRFRKRKMHVFEYCDHTLLNELRNPNVGADGVKSVLWOTLOALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Db 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Qy 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELTSSDPPA 240
 Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELTSSDPPA 240
 Qy 218 -----GKLPRHQSIFKSNFGFHGISIPEDMETLEEKFSVHPVFNFMKGLK 268
 Db 241 VASQSAGITGKLIPRHQSIFKSNFGFHGISIPEDMETLEEKFSVHPVFNFMKGLK 300
 Qy 269 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNRNRQVLPKLS 315
 Db 301 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNRNRQVLPKLS 347

RESULT 4

US-09-671-050-4
 ; Sequence 4, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-4

Query Match 97.0%; Score 1612; DB 4; Length 356;
 Best Local Similarity 90.6%; Pred. No. 2.4e-161;
 Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60

Db 1 MEKYEKLAKTCEGSGVGVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHH 120
Db 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHH 120
Qy 121 NCIRDIKPENILITKQIHKICDFGFAQILI-PGDATYDVATRWYRAPELLVGDTOYGS 180
Db 121 NCIRDIKPENILITKQIHKICDFGFAQILI-PGDATYDVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTL----- 217
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSPPA 240
Qy 218 -----GKLI PRHQSIFKSNFGFFHGISIPEDMETLEEKFSVDHPVAFNMFKGCLK 268
Db 241 VASQSAGITGKLI PRHQSIFKSNFGFFHGISIPEDMETLEEKFSVDHPVAFNMFKGCLK 300
Qy 269 MNPDDLRTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQOV 310
Db 301 MNPDDLRTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQOV 342

RESULT 5
US-09-949-016-7552
; Sequence 7552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7552
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7552

Query Match 71.5%; Score 1188.5; DB 4; Length 367;
Best Local Similarity 70.5%; Pred. No. 1.1e-116;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTCEGSGVGVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 11 MEKYEKGKIGEGSGVGVFKCRNRTQGIIVAIKFFLESEDDPVVKKIALREIRMLKQLKH 70
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHH 120
Db 71 PNLVNLIEVFRKRKMLHVFYCDHTVHLEDRYQGVPEHLVKSITWQTLQAVNFCHH 130
Qy 121 NCIRDIKPENILITKQIHKICDFGFAQILI-PGDATYDVATRWYRAPELLVGDTOYGS 179
Db 131 NCIRDIKPENILITKHSVIKLCDFGFAELLTGSDYVTDYVATRWYRSPPELLVGDTOYGS 190
Qy 180 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLGLKLI PRHQSIFKSNFGFFHGISI 239
Db 191 PPVDVWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLGLDIPRHQQVVFSTNQYFSGVKI 250
Qy 240 PEPEDMETLEEKFSVDHPVAFNMFKGCLKNPDDLRTCSQLLESSYFDSFOEAQIKRKAR 299
Db 251 PDPEDMEPLELKFNPISYPALGLUKGCLHMDPTELRITCEQLLHHHPYFENIREIDLAKH 310

Qy 300 NE 301
Db 311 NK 312
RESULT 6
US-09-411-628-11
; Sequence 11, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-628-11

Query Match 71.2%; Score 1183.5; DB 4; Length 358;
Best Local Similarity 71.8%; Pred. No. 3.6e-116;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTCEGSGVGVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 2 MEKYEKGKIGEGSGVGVFKCRNRTQGIIVAIKFFLESEDDPVVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHH 120
Db 62 PNLVNLIEVFRKRKMLHVFYCDHTVHLEDRYQGVPEHLVKSITWQTLQAVNFCHH 121
Qy 121 NCIRDIKPENILITKQIHKICDFGFAQILI-PGDATYDVATRWYRAPELLVGDTOYGS 179
Db 122 NCIRDIKPENILITKHSVIKLCDFGFAELLTGSDYVTDYVATRWYRSPPELLVGDTOYGS 181
Qy 180 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLGLKLI PRHQSIFKSNFGFFHGISI 239
Db 182 PPVDVWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLGLDIPRHQQVVFSTNQYFSGVKI 241
Qy 240 PEPEDMETLEEKFSVDHPVAFNMFKGCLKNPDDLRTCSQLLESSYFDSFOEAQ 293
Db 242 PDPEDMEPLELKFNPISYPALGLUKGCLHMDPTELRITCEQLLHHHPYFENIREIE 295

RESULT 7
US-10-174-794-11
; Sequence 11, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-11


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7954
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7954

Query Match      56.6%; Score 941.5; DB 4; Length 475;
Best Local Similarity 53.1%; Pred. No. 1.9e-90;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIMLKQLKH 60
Db 3 MEKYNLGLVGEKSGYGVVFKCRNKTGRIVAIFKFLFESDDDKMVKIAMREIKLKQLRH 62
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 63 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQKYLFIINGIGFCHSH 122
Qy 121 NCIRDIKPENILITKOGIIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDVKYG 182
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLI PRHQSIFKSNGFHGISI 239
Db 183 KAVDVWAIGCLVTEMFMGEPLFPDGSDDIDQLYHIMMCLGNLIPRHQELFNKNPVFAGVRL 242
Qy 240 PEPEDMETLEEKFSVHPVALNFMKGLKMPDRLTCSOLLESSYF--DSF-----QEA 292
Db 243 PEIKEREPLERRYPKLSEVVIDLAKCLHIDPDKRPFCAELLHHDDFFQMDGFAERFSQEL 302
Qy 293 QIK--RKARN-----EGRNRRRQ 309
Db 303 QLKVKQDARNVSLSKSKSQRKKEK 326

RESULT 11
US-09-411-628-10
; Sequence 10, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-628-10

Query Match      56.6%; Score 941.5; DB 4; Length 493;
Best Local Similarity 53.1%; Pred. No. 1.9e-90;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIMLKQLKH 60
Db 1 MEKYNLGLVGEKSGYGVVFKCRNKTGRIVAIFKFLFESDDDKMVKIAMREIKLKQLRH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 63 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQKYLFIINGIGFCHSH 120
Qy 121 NCIRDIKPENILITKOGIIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDVKYG 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLI PRHQSIFKSNGFHGISI 239
Db 183 KAVDVWAIGCLVTEMFMGEPLFPDGSDDIDQLYHIMMCLGNLIPRHQELFNKNPVFAGVRL 242
Qy 240 PEPEDMETLEEKFSVHPVALNFMKGLKMPDRLTCSOLLESSYF--DSF-----QEA 292
Db 243 PEIKEREPLERRYPKLSEVVIDLAKCLHIDPDKRPFCAELLHHDDFFQMDGFAERFSQEL 302
Qy 293 QIK--RKARN-----EGRNRRRQ 309
Db 303 QLKVKQDARNVSLSKSKSQRKKEK 326

RESULT 12
US-10-174-794-10
; Sequence 10, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-10

Query Match      56.6%; Score 941.5; DB 4; Length 493;
Best Local Similarity 53.1%; Pred. No. 1.9e-90;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIMLKQLKH 60
Db 1 MEKYNLGLVGEKSGYGVVFKCRNKTGRIVAIFKFLFESDDDKMVKIAMREIKLKQLRH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 63 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQKYLFIINGIGFCHSH 120
Qy 121 NCIRDIKPENILITKOGIIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDVKYG 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLI PRHQSIFKSNGFHGISI 239
Db 183 KAVDVWAIGCLVTEMFMGEPLFPDGSDDIDQLYHIMMCLGNLIPRHQELFNKNPVFAGVRL 242
Qy 240 PEPEDMETLEEKFSVHPVALNFMKGLKMPDRLTCSOLLESSYF--DSF-----QEA 292
Db 243 PEIKEREPLERRYPKLSEVVIDLAKCLHIDPDKRPFCAELLHHDDFFQMDGFAERFSQEL 302
Qy 293 QIK--RKARN-----EGRNRRRQ 309
Db 303 QLKVKQDARNVSLSKSKSQRKKEK 326

RESULT 13
US-09-671-050-2
; Sequence 2, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael

```

APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
FILE REFERENCE: Lex-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/156,511
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 187
TYPE: PRT
ORGANISM: homo sapiens
US-09-671-050-2

Query Match 47.6%; Score 791; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIIHRDIKPENILITKQGIKICDPGFAQIL 151
DB 121 NCIIHRDIKPENILITKQGIKICDPGFAQIL 151

RESULT 14
US-09-671-050-8
Sequence 8, Application US/09671050
Patent No. 6716616
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
FILE REFERENCE: Lex-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/156,511
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 198
TYPE: PRT
ORGANISM: homo sapiens
US-09-671-050-8

Query Match 47.6%; Score 791; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.6e-75;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADVGVKSVLWQTLQALNFCIH 120

QY 121 NCIIHRDIKPENILITKQGIKICDPGFAQIL 151
DB 121 NCIIHRDIKPENILITKQGIKICDPGFAQIL 151
RESULT 15
US-09-538-092-1236
Sequence 1236, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapadSeqFormatter Version 0.9
SEQ ID NO 1236
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q00526
US-09-538-092-1236

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Best Local Similarity 39.8%; Pred. No. 9.4e-53;
Matches 123; Conservative 66; Mismatches 96; Indels 24; Gaps 8;
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DB 1 MDMFQKVEKIGEGTVGVVYKAKNREGQLVAKKIRLDEMEGVPESTAREISLLKE 57
QY 58 LKHPNVLNLIIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADVGVKSVLWQTLQALNF 116
DB 58 LKHPNVLNLIIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADVGVKSVLWQTLQALNF 117
QY 117 CHHNCIHRDIKPENILITKQGIKICDPGFAQIL-IPGDAYTDVAVFWYAPPELLVCD 175
DB 118 CHSHRVHRDLAPQNLINELGAIKLADFLARAFGVPLRTYTHVVTWLYRAPILLGS 177
QY 176 TOYGSVDIWAIGCVFAELLTQGPLMGKSDVDQLYLIIRTLGKLIIPRHQSIFKSNPFH 235
DB 178 KEYTTAVDIWSIGCIFAEWVTRKALFPGDSEIDQLFRIFRMLGT-----PSEDTPW 228
QY 236 GIS-IPE-----PE-DMETLEKFSDVHPVALNFMKGCILKMPDRLTCSQLLESSYFDS 288
DB 229 GVTQLPDYKSGSPKWKTRGLEIEVFNLEPEGRDLMLQLLOYDPSQRIITAKTALAHYPFSS 288
QY 289 FOEAQIKRK 297
DB 289 PEPSPAARQ 297

Search completed: April 22, 2005, 06:52:57
Job time : 31.929 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 06:50:50 ; Search time 780.363 Seconds
(without alignments)
134.334 Million cell updates/sec

Title: US-10-766-691-12

Perfect score: 1662

Sequence: 1 MEKYEKLKTGEGSYGVFK.....RKARNEGRRRQOVLPLKS 315

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1662	100.0	315	17	US-10-766-691-12
2	1639	98.6	342	15	US-10-333-314-10
3	1638	98.6	324	17	US-10-766-691-10
4	1636	98.4	347	17	US-10-766-691-10
5	1612	97.0	356	17	US-10-766-691-4
6	1188.5	71.5	358	15	US-10-363-616-391
7	1186.5	71.4	338	16	US-10-664-421-97
8	1183.5	71.2	358	14	US-10-174-794-11
9	1140	68.6	228	9	US-09-834-496A-2
10	967.5	58.2	566	14	US-10-174-794-4
11	941.5	56.6	493	14	US-10-174-794-10
12	941.5	56.6	493	15	US-10-369-022-22
13	941.5	56.6	493	16	US-10-757-262-108

14	791	47.6	187	17	US-10-766-691-2	Sequence 2, Appli
15	791	47.6	198	17	US-10-766-691-8	Sequence 8, Appli
16	784.5	47.2	455	16	US-10-620-052A-34	Sequence 34, Appli
17	712.5	42.9	154	16	US-10-250-889-62	Sequence 62, Appli
18	581	35.0	305	15	US-10-394-322A-8	Sequence 8, Appli
19	581	35.0	305	16	US-10-408-765A-544	Sequence 544, App
20	581	35.0	305	16	US-10-620-052A-20	Sequence 20, Appli
21	570	34.3	298	9	US-09-771-161A-187	Sequence 187, App
22	570	34.3	544	14	US-10-072-036-113	Sequence 113, App
23	570	34.3	544	14	US-10-072-036-115	Sequence 115, App
24	569	34.2	298	14	US-10-174-794-13	Sequence 13, Appli
25	569	34.2	298	14	US-10-295-681-27	Sequence 27, Appli
26	567	34.1	298	11	US-09-969-034-4493	Sequence 4493, Ap
27	567	34.1	298	15	US-10-394-322A-7	Sequence 7, Appli
28	567	34.1	298	16	US-10-620-052A-55	Sequence 55, Appli
29	567	34.1	298	16	US-10-664-421-14	Sequence 14, Appli
30	567	34.1	298	16	US-10-664-421-51	Sequence 51, Appli
31	565.5	34.0	297	14	US-10-295-681-51	Sequence 51, Appli
32	564	33.9	294	15	US-10-334-143-181	Sequence 181, Appli
33	563	33.9	298	14	US-10-295-681-31	Sequence 31, Appli
34	563	33.9	298	14	US-10-295-681-39	Sequence 39, Appli
35	561.5	33.8	294	15	US-10-389-566-1333	Sequence 1333, Ap
36	561	33.8	298	14	US-10-295-681-29	Sequence 29, Appli
37	561	33.8	298	14	US-10-295-681-43	Sequence 43, Appli
38	559	33.6	298	14	US-10-295-681-35	Sequence 35, Appli
39	556.5	33.5	294	15	US-10-389-566-1030	Sequence 1030, Ap
40	556	33.5	297	14	US-10-060-065-11	Sequence 11, Appli
41	556	33.5	297	14	US-10-059-585-32	Sequence 32, Appli
42	556	33.5	297	14	US-10-177-293-41	Sequence 41, Appli
43	556	33.5	297	14	US-10-174-794-12	Sequence 12, Appli
44	556	33.5	297	14	US-10-204-041-8	Sequence 8, Appli
45	556	33.5	297	15	US-10-394-322A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-766-691-12
; Sequence 12, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 315
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-12

Query Match 100.0%; Score 1662; DB 17; Length 315;
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QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIRHDIKPENILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRHDIKPENILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNGFHGISIP 240
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNGFHGISIP 240
QY 241 EPEDMETLEEFSDVHPVAFNFMKGLKXNPPDRITCSQLESSEYFDSFOEAQIKRKARN 300
DB 241 EPEDMETLEEFSDVHPVAFNFMKGLKXNPPDRITCSQLESSEYFDSFOEAQIKRKARN 300
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DB 301 EGRNRRQVPLKS 315

RESULT 2

US-10-333-314-10

; Sequence 10, Application US/10333314

; Publication No. US20030211093A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry

; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal

; APPLICANT: HAPALIA, April J.A.; CHAWLA, Narinder K.

; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi

; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.

; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.

; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga

; APPLICANT: NGUYEN, Daniel B.; LU, Yan

; APPLICANT: BURFORD, Neil; LAL, Preeti G.

; APPLICANT: DING, Li; YAO, Monique G.

; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.

; APPLICANT: KEARNEY, Liam; LU, Dying Aina M.

; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom

; APPLICANT: XU, Yuming; WALSH, Roderick T.

; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming

; APPLICANT: JACKSON, Jennifer L.

; TITLE OF INVENTION: HUMAN KINASES

; FILE REFERENCE: PI-0162 USN

; CURRENT APPLICATION NUMBER: US/10/333,314

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: PCT/US01/23092

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/220,038

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/222,112

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,831

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/224,729

; PRIOR FILING DATE: 2000-08-11

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PERL Program

; SEQ ID NO 10

; LENGTH: 342

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 1698381CD1

US-10-333-314-10

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Best Local Similarity 99.0%; Pred. No. 1.9e-130;
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DB 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIRHDIKPENILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRHDIKPENILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNGFHGISIP 240
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNGFHGISIP 240
QY 241 EPEDMETLEEFSDVHPVAFNFMKGLKXNPPDRITCSQLESSEYFDSFOEAQIKRKARN 300
DB 241 EPEDMETLEEFSDVHPVAFNFMKGLKXNPPDRITCSQLESSEYFDSFOEAQIKRKARN 300
QY 301 EGRNRRQVPL 313
DB 301 EGRNRRQVPL 315

RESULT 3

US-10-766-691-6

; Sequence 6, Application US/10766691

; Publication No. US20050042626A1

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: Novel Human Kinase Proteins and

; TITLE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0046-USA

; CURRENT APPLICATION NUMBER: US/10/766,691

; PRIOR FILING DATE: 2004-01-28

; PRIOR APPLICATION NUMBER: US/09/671,050

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US 60/156,511

; PRIOR FILING DATE: 1999-09-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 324

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-766-691-6

Query Match 98.6%; Score 1638; DB 17; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.2e-130;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIRHDIKPENILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRHDIKPENILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNGFHGISIP 240
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNGFHGISIP 240
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RESULT 5
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; Sequence 4, Application US/10766691
; Publication No. US2005042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander J
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn

Query Match 71.5%; Score 1188.5; DB 15; Length 358;
Best Local Similarity 70.5%; Pred. No. 2.7e-92;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1

Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60

Db 2 MEKYEKIGIGEGSYGVVFKCRNRDTGQIVAIKKFLESDDPVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELERNPNGVADGVKSVLWOTLOALNFCIH 120
Db 62 PNLVNLIEVFRKRRKMLHVEYCDHTVLHLDYRQGVPEHLVKSITWOTLOAVNFCXH 121
Qy 121 NCIRDIPKPNILITKOGIIKICDFGFAQLI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
Db 122 NCIRDIPKPNILITKOGIIKICDFGFAQLI-PGDAYTDYVATRYRPAPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSVDOLYLIIRTLGKLIPRHOSIFKSNFGPHGISI 239
Db 182 PPVDVWAIGCVFAELLTGQPLWPKGSVDOLYLIIRTLGKLIPRHOSIFKSNFGPHGISI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMKGLKMPDRDLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PEPEDMETLEKFSVDHPVAFNMKGLKMPDRDLTCSQLLESSYFDSFQEAQIKRKAR 301
Qy 300 NE 301
Db 302 NK 303

RESULT 7

US-10-664-421-97
; Sequence 97, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-97

Query Match 71.4%; Score 1186.5; DB 16; Length 338;
Best Local Similarity 70.5%; Pred. No. 3.8e-92;
Matches 213; Conservative 41; Mismatches 47; Indels 1; Gaps 1;
Qy 1 MEKYEKIAKTGEGSYGVVFKCRNRDTGQIVAIKKFLESDDPVKKIALREIRMLKQLKH 60
Db 2 MEKYEKIGIGEGSYGVVFKCRNRDTGQIVAIKKFLESDDPVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELERNPNGVADGVKSVLWOTLOALNFCIH 120
Db 62 PNLVNLIEVFRKRRKMLHVEYCDHTVLHLDYRQGVPEHLVKSITWOTLOAVNFCXH 121
Qy 121 NCIRDIPKPNILITKOGIIKICDFGFAQLI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
Db 122 NCIRDIPKPNILITKOGIIKICDFGFAQLI-PGDAYTDYVATRYRPAPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSVDOLYLIIRTLGKLIPRHOSIFKSNFGPHGISI 239
Db 182 PPVDVWAIGCVFAELLTGQPLWPKGSVDOLYLIIRTLGKLIPRHOSIFKSNFGPHGISI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMKGLKMPDRDLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PEPEDMETLEKFSVDHPVAFNMKGLKMPDRDLTCSQLLESSYFDSFQEAQIKRKAR 301

Qy 300 NE 301
Db 302 NK 303

RESULT 8

US-10-174-794-11
; Sequence 11, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-11

Query Match 71.2%; Score 1183.5; DB 14; Length 358;
Best Local Similarity 71.8%; Pred. No. 7.2e-92;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MEKYEKIAKTGEGSYGVVFKCRNRDTGQIVAIKKFLESDDPVKKIALREIRMLKQLKH 60
Db 2 MEKYEKIGIGEGSYGVVFKCRNRDTGQIVAIKKFLESDDPVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELERNPNGVADGVKSVLWOTLOALNFCIH 120
Db 62 PNLVNLIEVFRKRRKMLHVEYCDHTVLHLDYRQGVPEHLVKSITWOTLOAVNFCXH 121
Qy 121 NCIRDIPKPNILITKOGIIKICDFGFAQLI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
Db 122 NCIRDIPKPNILITKOGIIKICDFGFAQLI-PGDAYTDYVATRYRPAPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSVDOLYLIIRTLGKLIPRHOSIFKSNFGPHGISI 239
Db 182 PPVDVWAIGCVFAELLTGQPLWPKGSVDOLYLIIRTLGKLIPRHOSIFKSNFGPHGISI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMKGLKMPDRDLTCSQLLESSYFDSFQEAQ 293
Db 242 PEPEDMETLEKFSVDHPVAFNMKGLKMPDRDLTCSQLLESSYFDSFQEAQ 295

RESULT 9

US-09-834-496A-2
; Sequence 2, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 38155200900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-496A-2


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; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/387,536
; PRIOR FILING DATE: 2002-06-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-022-22
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Query Match 56.6%; Score 941.5; DB 15; Length 493;
Best Local Similarity 53.1%; Pred. No. 3.2e-71;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

QY 1 MEKYEKLATGSGYGVFEKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYNELGLVSGSGYGMWCKRKTGRIVAIFKFLSDDDKMKVKIAMREIKLLQLRH 60
QY 61 PNLVNLIEVFRKRKMHVLFVEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKRWYLVFEVDHTILDDLEFNGLDYQVQKYLFIQINGIFGCHSH 120
QY 121 NCIHRIKIPENILITKQGIKICDFGPAQIL-IPGDATDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRIKIPENILVSQSGVVKLCDFGFARTLAAPGEVTDYVATRWYRAPELLVGDVKY 180
QY 180 SSVDTWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHOSIFKSNRFFHGISI 239
Db 181 KAVDVWAIGCLVTENFMGEPLFGDSDIDQLYHIMMCLGNLIPRHQELFNKNPVFAGVRL 240
QY 240 PEPEDMETLEKFSVDVHPVAFNMFKGCKLWMPDRLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLRRYPKLSVWIDLAKKCHLHIDPKRPFCAELLHHDFFOMDGFARFSQEL 300
QY 293 QIK--RKARN-----EGNRRRQ 309
Db 301 QLKVKQDARNVSLSKSKSNRKKK 324
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RESULT 13
US-10-757-262-108
; Sequence 108, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 30013, 32678 OR
; TITLE OF INVENTION: 55053
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; FILE REFERENCE: MPI03-007PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-108
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Query Match 56.6%; Score 941.5; DB 16; Length 493;
Best Local Similarity 53.1%; Pred. No. 3.2e-71;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

QY 1 MEKYEKLATGSGYGVFEKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYNELGLVSGSGYGMWCKRKTGRIVAIFKFLSDDDKMKVKIAMREIKLLQLRH 60
QY 61 PNLVNLIEVFRKRKMHVLFVEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKRWYLVFEVDHTILDDLEFNGLDYQVQKYLFIQINGIFGCHSH 120
QY 121 NCIHRIKIPENILITKQGIKICDFGPAQIL-IPGDATDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRIKIPENILVSQSGVVKLCDFGFARTLAAPGEVTDYVATRWYRAPELLVGDVKY 180
QY 180 SSVDTWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHOSIFKSNRFFHGISI 239
Db 181 KAVDVWAIGCLVTENFMGEPLFGDSDIDQLYHIMMCLGNLIPRHQELFNKNPVFAGVRL 240
QY 240 PEPEDMETLEKFSVDVHPVAFNMFKGCKLWMPDRLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLRRYPKLSVWIDLAKKCHLHIDPKRPFCAELLHHDFFOMDGFARFSQEL 300
QY 293 QIK--RKARN-----EGNRRRQ 309
Db 301 QLKVKQDARNVSLSKSKSNRKKK 324
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RESULT 14
US-10-766-691-2
; Sequence 2, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
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FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/10/766.691
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 187
TYPE: PRT
ORGANISM: homo sapiens
US-10-766-691-2

Query Match 47.6%; Score 791; DB 17; Length 187;
Best Local Similarity 100.0%; Pred. No. 5.6e-59;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Qy 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151
Db 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151

RESULT 15

US-10-766-691-8
Sequence 8, Application US/10766691
Publication No. US20050042626A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Kinase Proteins and
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/10/766.691
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 198
TYPE: PRT
ORGANISM: homo sapiens
US-10-766-691-8

Query Match 47.6%; Score 791; DB 17; Length 198;
Best Local Similarity 100.0%; Pred. No. 6e-59;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Qy 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151

Db 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151
Search completed: April 22, 2005, 07:36:43
Job time : 781.363 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 06:47:40 ; Search time 14.2749 Seconds
(without alignments)
1576.747 Million cell updates/sec

Title: US-10-766-691-12

Perfect score: 1562

Sequence: 1 MEKYEKLAKTGGSYGVVFK.....RKARNEGRNRROQVLPKS 315

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 314081 seqs, 71453778 residues

Total number of hits satisfying chosen parameters: 314081

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1504	90.5	485	1	PCT-US05-03526-7
2	1183.5	71.2	338	1	PCT-US04-30360-97
3	1183.5	71.2	338	6	US-10-941-635-97
4	941.5	56.6	493	1	PCT-US05-03526-5
5	909	54.7	350	8	US-60-655-875-129900
6	784.5	47.2	455	1	PCT-US05-03526-6
7	720.5	43.4	1030	1	PCT-US05-03526-8
8	569	34.2	224	6	US-10-450-763-36501
9	567	34.1	298	1	PCT-US04-30360-14
10	567	34.1	298	1	PCT-US04-30360-51
11	567	34.1	298	6	US-10-941-635-51
12	567	34.1	298	6	US-10-941-635-51
13	567	34.1	298	7	US-11-021-951-168
14	561.5	33.8	294	8	US-60-643-717-18889
15	555.5	33.4	300	8	US-60-643-717-7327
16	555.5	33.4	300	8	US-60-643-717-7328
17	554.5	33.4	294	8	US-60-643-717-9856
18	551.5	33.2	294	8	US-60-643-717-9196
19	550.5	33.1	294	8	US-60-643-717-1362
20	549.5	33.1	294	8	US-60-643-717-11788
21	549.5	33.1	294	8	US-60-643-717-12472
22	549.5	33.1	294	8	US-60-643-717-17436
23	547.5	32.9	294	8	US-60-643-717-3546
24	544.5	32.8	290	8	US-60-643-717-10996
25	544.5	32.8	294	8	US-60-643-717-10239

26	542.5	32.6	294	8	US-60-643-717-14313	Sequence 14313, A
27	542.5	32.6	294	8	US-60-643-717-14791	Sequence 14791, A
28	541.5	32.6	294	8	US-60-643-717-11662	Sequence 11662, A
29	540.5	32.5	294	8	US-60-643-717-13623	Sequence 13623, A
30	539.5	32.5	294	8	US-60-643-717-15844	Sequence 15844, A
31	536.5	32.3	298	8	US-60-643-717-16355	Sequence 16355, A
32	530.5	31.9	345	1	PCT-US04-30360-71	Sequence 71, Appl
33	530.5	31.9	345	6	US-10-941-635-71	Sequence 71, Appl
34	525.5	31.6	341	8	US-60-643-717-16441	Sequence 16441, A
35	522	31.4	293	8	US-60-643-717-14335	Sequence 14335, A
36	522	31.4	326	8	US-60-643-717-8068	Sequence 8068, Ap
37	520.5	31.3	303	8	US-60-643-717-16553	Sequence 16553, A
38	517	31.1	304	8	US-60-643-717-14840	Sequence 14840, A
39	516.5	31.1	291	8	US-60-643-717-18659	Sequence 18659, A
40	515	31.0	303	8	US-60-643-717-3781	Sequence 3781, Ap
41	514.5	31.0	280	8	US-60-643-717-15222	Sequence 15222, A
42	511.5	30.8	307	8	US-60-643-717-3350	Sequence 3350, Ap
43	509.5	30.7	379	8	US-60-643-717-11541	Sequence 11541, A
44	505.5	30.4	317	8	US-60-643-717-17906	Sequence 17906, A
45	505.5	30.4	527	7	US-11-033-515-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US05-03526-7
; Sequence 7, Application PC/TUS0503526
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MEMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
; FILE REFERENCE: EX05-003C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03526
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,835
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US05-03526-7

Query Match 90.5%; Score 1504; DB 1; Length 485;
Best Local Similarity 91.9%; Pred. No. 9.8e-89;
Matches 294; Conservative 6; Mismatches 14; Indels 6; Gaps 2;

Qy	2	EKYEKLAKTGGSYGVVFKCRNKTSGQVAVKKEVSEDDPVVKKIALREIRMLKQLKHP	61
Db	166	DPYEKLAKTGGSYGVVFKCRNKTSGQVAVKKEVSEDDPVVKKIALREIRMLKQLKHP	225
Qy	62	NLVNLIIEVFRKRKMHVFEYCDHTLNELEARNPNGVAD---GVIKSVLWQTLOA---LN	115
Db	226	NLVNLIIEVFRKRKMHVFEYCDHTLNELEARNPNGVADSDSIVGRLSVADRSLAPKKN	285
Qy	116	FCIHNCIHRDKPENILITKQGIKICDFGAQILIPGDAYTDYVATRWYRAPELLVGD	175
Db	286	QIMLQCIHRDKPENILITKQGIKICDFGAQILIPGDAYTDYVATRWYRAPELLVGD	345
Qy	176	TOYGVSSVDIWAIGCVFAELLTQGPLWFGKSDVDLYLIIRTLGKLIIRHQIFKNSGFFH	235
Db	346	TOYGVSSVDIWAIGCVFAELLTQGPLWFGKSDVDLYLIIRTLGKLIIRHQIFKNSGFFH	405
Qy	236	GISTPEPEDMETLEKEFSDVHPVAFNMKGLKKNPDRLTCSQLLESSYFDSFOEAQIK	295
Db	406	GISTPEPEDMETLEKEFSDVHPVAFNMKGLKKNPDRLTCSQLLESSYFDSFOEAQIK	465
Qy	296	RKARNEGRNRROQVLPKS	315
Db	466	RKARNEGRNRROQVLPKS	485

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RESULT 2
PCT-US04-30360-97
; Sequence 97, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-97

Query Match      71.2%; Score 1183.5; DB 1; Length 338;
Best Local Similarity 71.8%; Pred. No. 1.8e-68;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRTGQIVAKKFLSEDDPVVKKIALREIRMLKOLKH 61
QY 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELRNPNGVADGVKISVLWQTLQALNFCCHI 120
Db 62 PNLVNLLEVFRKRRLHVLVEYCDHTVLHELDYQGVPEHLVKSITWTQLQAVNFCCHK 121
QY 121 NCIHRIKPENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 122 NCIHADVAPENILITKHSVIKLCDFGFARLTGFSYDYYTDYVATRWYRSPPELLVGDTOYG 181
QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGKLIIPRHQSIFKSNPFHGISI 239
Db 182 PPVDVWAIGCVFAELLGSGVPLWPKGSDVDQYLIIRKTLGDLIIPRHQQVFTNQYFSGVKI 241
QY 240 PEPEDMETLEKFSVDVHPVAFNFMKGLKMPDRDLTCSQLLESSYFDSFOEAQ 293
Db 242 PDPEDMEPLEKFPNISYPALGKLLKGLHMDPTERLTCEQLLHHPYFENIREIE 295

RESULT 3
US-10-941-635-97
; Sequence 97, Application US/10941635
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-97
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Query Match      71.2%; Score 1183.5; DB 6; Length 338;
Best Local Similarity 71.8%; Pred. No. 1.8e-68;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRTGQIVAKKFLSEDDPVVKKIALREIRMLKOLKH 61
QY 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELRNPNGVADGVKISVLWQTLQALNFCCHI 120
Db 62 PNLVNLLEVFRKRRLHVLVEYCDHTVLHELDYQGVPEHLVKSITWTQLQAVNFCCHK 121
QY 121 NCIHRIKPENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 122 NCIHADVAPENILITKHSVIKLCDFGFARLTGFSYDYYTDYVATRWYRSPPELLVGDTOYG 181
QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGKLIIPRHQSIFKSNPFHGISI 239
Db 182 PPVDVWAIGCVFAELLGSGVPLWPKGSDVDQYLIIRKTLGDLIIPRHQQVFTNQYFSGVKI 241
QY 240 PEPEDMETLEKFSVDVHPVAFNFMKGLKMPDRDLTCSQLLESSYFDSFOEAQ 293
Db 242 PDPEDMEPLEKFPNISYPALGKLLKGLHMDPTERLTCEQLLHHPYFENIREIE 295

RESULT 4
PCT-US05-03526-5
; Sequence 5, Application PC/TUS0503526
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MEMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
; FILE REFERENCE: EX05-003C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03526
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,835
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
PCT-US05-03526-5

Query Match      56.6%; Score 941.5; DB 1; Length 493;
Best Local Similarity 53.1%; Pred. No. 6.4e-53;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYENGLVGEYSYGVVWVKCRNKTGRIVAKKFLSEDDDDKWKVKIARREIKLKQURH 60
QY 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELRNPNGVADGVKISVLWQTLQALNFCCHI 120
Db 61 ENLVNLLEVCCKKRWLVLPFVDHTILDLELFPNGLDYQVVKYLFQINGIGFCHSH 120
QY 121 NCIHRIKPENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRIKPENILVVSQSGVVKLCDFGFARTLAAPGEVYTDYVATRWYRAPELLVGDVRYG 180
QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGKLIIPRHQSIFKSNPFHGISI 239
Db 181 KAVDVWAIGCVLTEMFMGEPLFPFGSDIDQLYHIMCGLNLIIPRQELFNKNPVPAGVRL 240
QY 240 PEPEDMETLEKFSVDVHPVAFNFMKGLKMPDRDLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLERRYPKLVSEVWIDLAKKKLHIDPDKPFCALLHHDDFQMDGFAERFSOEL 300
QY 293 QIK--RKARN-----EGRNRRRQ 309
Db 301 QLKVKQKDARNVSLSKSKSNRKKKEK 324
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Db 70 ENIVELKEAFRRRGLKYLVEYVEKNMELLEEMPGVPPEKVKSYIQLIKAIHWCHKN 129
Qy 121 NCIHRIKIPENILITKQGIKICDGFQAOLIPGD--AYTDYVATWYRAPPELLVGDQY 178
Db 130 DIVHRDIKIPENILISHNDVLUKCDGFARNLSGNNANYTEYVATWYRSPPELLG-APY 188
Qy 179 GSSVDIWAICVFAELLTGQPLWFGKSDVDQLYLIIRTLGKLIPIRHSQIFKSGNRPFGHS 238
Db 189 GKSVDMSVGCILGELSDGQPLFPGESEIDQLFTIQKVLGPLPSEQMKLYFNPRFHGUR 248
Qy 239 IPRPEDEMETLEEFSDV-HPVALNFMKGCLOMPDDRLTCSQLLESSYFDSQEAQIKRK 297
Db 249 FPAVNHQSLERYGLNLSVLLDMKNLKLDPADRYLTEQCLN---HPTFOTQRLDDR 305
Qy 298 ARNEGRNRNRQOV 310
Db 306 SPERSAKRKYHV 318

RESULT 8

US-10-450-763-36501
; Sequence 36501, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36501
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (115)..(146)
; OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
; OTHER INFORMATION: by EMATRIX, accession number BL00107A, p-value=8.500e-27, raw
; OTHER INFORMATION: score of 18.39
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (4)..(180)
; OTHER INFORMATION: Eukaryotic protein kinase domain identified by Pfam,
; OTHER INFORMATION: accession name pkinase, E-value=3.5e-65, Pfam score of 230.0
US-10-450-763-36501

Query Match 34.2%; Score 569; DB 6; Length 224;
Best Local Similarity 59.4%; Pred. No. 1.6e-29;
Matches 107; Conservative 32; Mismatches 39; Indels 2; Gaps 2;

Qy 1 MEKYELAKTGEISYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Db 1 MEMETLCKVGEISYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 59
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNLELRNPNGVADGVTKSVLWQTLQALNFCHTH 120
Db 60 ENLVNLIEVFRKQKHLVFEFDHTVLDLQHYCHGLSKRLRYKYLFOILRAIDYLSN 119
Qy 121 NCIHRIKIPENILITKQGIKICDGFQAOLIPGDYTDYVATWYRAPPELLVGDQY 179
Db 120 NIIHRDIKIPENILVSOGITKLCDFGARTLAAPGDYTDYVATWYRAPPELLVGDQY 179

RESULT 9

PCT-US04-30360-14
; Sequence 14, Application PC/TUS0430360

; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-14

Query Match 34.1%; Score 567; DB 1; Length 298;
Best Local Similarity 40.0%; Pred. No. 2.8e-29;
Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6;

Qy 1 MEKYELAKTGEISYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Db 1 MEMFQKEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIRISLLKELNH 60
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNLELRNP-NGVADGVTKSVLWQTLQALNFCFI 119
Db 61 PNIVKLLDVHTENKLYLVFEFLHQDLKKFMDASALTGIPLIKSYLFQLQGLAFCHS 120
Qy 120 HNCIHRIKIPENILITKQGIKICDGFQAOLIPGDYTDYVATWYRAPPELLVGDQY 178
Db 121 HRVLHRLDLPQNLINTEGAIKLADFLARAGVPVRYTTEHVVTLWYRAPELLGCKY 180
Qy 179 GSSVDIWAICVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPIRHSQIFKSGNFPFGI- 237
Db 181 STAVDIWSLGCIFAENVTRALPFGDSEIDQLFRIFRILGT-----PDEVVMPGVT 231
Qy 238 SIPE--PEMETLEKFSVDVHPV---ALNFMKGLKMNPPDRLTCSQLLESSYF 286
Db 232 SMPDYKSPFKWARQDFSKVVPPLDEDSRSLLSQMLHYDPNKRISAKAALAHPPF 286

RESULT 10

PCT-US04-30360-51
; Sequence 51, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 51
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-51

Query Match 34.1%; Score 567; DB 1; Length 298;
Best Local Similarity 40.0%; Pred. No. 2.8e-29;
Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6;

Qy 1 MEKYELAKTGEISYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKOLKH 60
Db 1 MEMFQKEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIRISLLKELNH 60


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; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 168
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-168

Query Match
Best Local Similarity 34.1%; Score 567; DB 7; Length 298;
Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6;

QY 1 MEKYELAKTGGSGVGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MENFOKVEKIGEGTYGVVYKARNKLTGEVVALKIRLDTETEGVPSTAIRISLLKELNH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNP-NGVADGVKSVLWQTLQALNFC 119
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNP-NGVADGVKSVLWQTLQALNFC 119
QY 120 HNCIHRDIKPNILITKOGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 178
DB 121 HRVLHRLKPNQLLNTGAIKADFLARAFGVPTVTHEVVTWYRAPELLVGD 180
QY 179 GSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIIPRHOSIFKSN 237
DB 181 STAVDILWSLGCIFAEWMTTRALFPDSEIDQIFRIFRTLTG- 231
QY 238 SIPE--PEDMETLEKFSVDHVPV----ALNFMKGLKXNPPDRLTCSQLLESSYF 286
DB 232 SMPDYKPSFKWARQDFSKVPPLEDGSRSLSQMLHVDPNKRISAKAALHPFF 286

RESULT 14
US-60-643-717-18889
; Sequence 18889, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 18889
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Saccharum officinarum
US-60-643-717-18889

Query Match
Best Local Similarity 33.8%; Score 561.5; DB 8; Length 294;
Matches 115; Conservative 69; Mismatches 92; Indels 35; Gaps 9;

QY 1 MEKYELAKTGGSGVGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MEQYKVEKIGEGTYGVVYKARNKLTGEVVALKIRLDTETEGVPSTAIRISLLKEMNH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPVGADGVKSVLWQTLQAL 114
DB 61 DNIVRLHDVHSEKRYLVFEFLDLDLKKFMDSCPEFAKNPT-----LIKSVLYQLRGV 115
QY 115 NFCHHNCIHRDIKPNILITKOGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELL 172
DB 116 AYCHSHRFLHRLKPNQLLIDRTNTLKLADFGLSRAFGIPVPTFHEVVTWYRAPELL 175
QY 173 VGDYQSGSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIIPRHOSIFK 232
DB 176 LGAKQYSTPVDVMSVGCIFAEWMTTRALFPDSEIDELFKIFRVLG--TPNEQS----- 227

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QY 233 FFHGIS-IP-----EPEDMETLEKFSVDHVPVVALNFMKGLKXNPPDRLTCSOLLE 282
DB 228 -WPGVSCLPDFKTAAPPWQAQDLATI---VNLFPAGLDLLSKMLRYEPSKRIARQAILE 283
QY 283 SSYFDSFQEAQ 293
DB 284 HEYFKDLEWVQ 294

RESULT 15
US-60-643-717-7327
; Sequence 7327, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 7327
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Pneumocystis carinii
US-60-643-717-7327

Query Match
Best Local Similarity 33.4%; Score 555.5; DB 8; Length 300;
Matches 113; Conservative 72; Mismatches 91; Indels 27; Gaps 8;

QY 1 MEKYELAKTGGSGVGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MEQYKVEKIGEGTYGVVYKARNKLTGEVVALKIRLDTETEGVPSTAIRISLLKEMNH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVGADG--VIKSVLWQTLQALNFC 118
DB 61 DNIVRLHNIHOESRLYLVFEFLDLDLKKYMNISIPKDMMLGAEMIKKFWSQLVSGVKYCH 120
QY 119 HNCIHRDIKPNILITKOGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 177
DB 121 SHRLHRLKPNQLLIDREGNKLADFLARAFGVPLRGYTHEVVTWYRAPELLVGRQ 180
QY 178 YGSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIIPRHOSIFKSN 237
DB 181 YATALDINSIGCIFAEWMTTRALFPDSEIDQIFRIFRTLTG-TPDENS-----WPGI 231
QY 238 -SIPE-----PEDM-ETLEKFSVDHVPVVALNFMKGLKXNPPDRLTCSQLLESSYF 286
DB 232 TSYPDFKATFPKWSPNLIGELITELSDS----GIDLLQKCLRYYPAAERISAKKALDHPYF 287
QY 287 DSF 289
DB 288 DDF 290

Search completed: April 22, 2005, 07:09:11
Job time : 15.2749 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 03:32:53 ; Search time 25.6949 Seconds
(without alignments)
1179.546 Million cell updates/sec

Title: US-10-766-691-12
Perfect score: 1662
Sequence: 1 MEKYEKLAKTGEISYGVFK.....RKARNEGRRRQQVLPLKS 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1183.5	71.2	358	2 S23383	protein kinase (EC
2	1175.5	70.7	376	2 S22745	serine/threonine p
3	581	35.0	305	2 S23382	protein kinase (EC
4	574.5	34.6	292	2 S40021	protein kinase (EC
5	571.5	34.4	294	1 A40444	protein kinase (EC
6	571.5	34.4	294	2 B40444	protein kinase (EC
7	570.5	34.3	302	1 S50474	protein kinase (EC
8	568.5	34.2	294	2 S22440	protein kinase (EC
9	567	34.1	298	2 A41227	protein kinase (EC
10	565.5	34.0	297	2 A37871	protein kinase (EC
11	561.5	33.8	294	2 S23095	protein kinase (EC
12	559	33.6	302	1 A43499	protein kinase (EC
13	557	33.5	297	1 S24913	protein kinase (EC
14	556.5	33.5	294	2 T49271	CELL DIVISION CONT
15	556	33.5	297	2 A29539	protein kinase (EC
16	556	33.5	297	2 T45977	cyclin-dependent k
17	556	33.5	302	2 B44349	protein kinase (EC
18	554	33.3	301	1 S19209	protein kinase (EC
19	553	33.3	298	1 A44878	protein kinase (EC
20	551.5	33.2	311	2 S36619	protein kinase (EC
21	551	33.2	288	1 S42566	protein kinase (EC
22	550.5	33.1	294	1 S57928	protein kinase (EC
23	550.5	33.1	294	1 J02243	protein kinase (EC
24	550.5	33.1	294	1 S42049	protein kinase (EC
25	547.5	32.9	303	1 S06011	protein kinase (EC
26	547.5	32.9	308	1 S53538	protein kinase (EC
27	546.5	32.9	297	1 S12009	protein kinase cdc
28	545	32.8	297	1 A46355	protein kinase (EC
29	544.5	32.8	291	2 S23386	protein kinase (EC

30	544	32.7	293	2 JE0374	cyclin-dependent k
31	543	32.7	292	1 A45091	protein kinase (EC
32	543	32.7	292	1 I49592	protein kinase (EC
33	543	32.7	297	1 A36074	protein kinase (EC
34	543	32.7	301	1 S42101	protein kinase (EC
35	541.5	32.6	294	1 S31332	protein kinase (EC
36	540	32.5	296	2 S24386	protein kinase (EC
37	539	32.4	302	1 OKB185	protein kinase PHO
38	535.5	32.2	302	2 T17115	protein kinase cdc
39	530.5	31.9	346	2 A54820	CDK-activating pro
40	530	31.9	294	2 S51008	protein kinase (EC
41	528	31.8	292	2 S22441	protein kinase (EC
42	527.5	31.7	346	2 A56231	MOL15/CDK-activat
43	527	31.7	346	1 I78840	protein kinase (EC
44	525	31.6	332	1 S41003	protein kinase (EC
45	525	31.6	346	1 I48157	protein kinase (EC

ALIGNMENTS

RESULT 1

S23383
protein kinase (EC 2.7.1.37) cdc2-related KKIALRE - human
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C/Accession: S23383; S22744
R:Mayerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai;
EMBO J. 11, 2909-2917, 1992
A:Title: A family of human cdc2-related protein kinases.
A:Reference number: S23382; MUID:92347325; PMID:1639063
A/Accession: S23383
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-358 <MEY>
A:Cross-references: UNIPROT:Q00532; EMBL:X66358; NID:G36614; PIDN:CAA47002.1; PID:G36615
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:3-278/Domain: protein kinase homology <KIN>
F:11-19/Region: protein kinase ATP-binding motif
F:34,52,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match	71.2%	Score 1183.5;	DB 2;	Length 358;
Best Local Similarity	71.8%;	Pred. No. 5.1e-48;		
Matches 211;	Conservative 41;	Mismatches 41;	Indels 1;	Gaps 1;
Qy	1	MEKYEKLAKTGEISYGVFKRNTSGQVAVKVFESDDPVVKIALREIRMLKQLKH	60	
Db	2	MEKYEKIGKIGESYGVFKRNRDTGQIVAKKFLSEDDPVVKIALREIRMLKQLKH	61	
Qy	61	PNLVNLEIEVFRKRKMLHVFYCDHTLLNLELRNPNGVADGVTKSVLWQTLQALNFCIH	120	
Db	62	PNLVNLEIEVFRKRRLHLVFYCDHTVLHLDYQYGVPEHLVKSITWQTLQAVNFCIKH	121	
Qy	121	NCIHRDKPENILITKQGIKICDFGFAQILI-PGDATYDVATRWYRAPPELLNGDTQYG	179	
Db	122	NCIHRDKPENILITKHSVIKLCDFGFARLLTGSDYYTQYVATRWYRSPELLNGDTQYG	181	
Qy	180	SSYDWAIGCVFAELLTGQPLWPKGSDVDQLYLIRTLGKLIPIRQHSIFKSNPFHGISI	239	
Db	182	PPVDWAIGCVFAELLSGVPLWPKGSDVDQLYLIRTKLGLDILPRHQVFSFNQYFSGVKI	241	
Qy	240	PEPEDMETLEKFSVDHPVAFNFMKGLKVNPPDRRLTCSQLLESSYFDSFQEAQ	293	
Db	242	PDPEDEMEPLEKFPNISYPALGGLKGLHMDPTERLTCEQLLHHHPYENIREIE	295	

RESULT 2

S22745
serine/threonine protein kinase KKIALRE (EC 2.7.1.1) - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997
C/Accession: S22745

A;Reference number: A40444; PMID:2014258
A;Accession: B40444

118 HIHNCIHRDIKPENILITKQIIKICDFGAQIL-IPGDAYTDYVATRWYRAPELLVGD 176 QY

Db 120 HCRVLRHDLKPNLLDNGKVIKLAFLGRLAFGVPRVYTHEVVTLMYRAPEVLGAS 179
 Qy 177 QYGSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLG-----KLIPRHOS 226
 Db 180 RYSPFVDSVIGTIFASLAKTKEFLHGDSEIDQLFRIFRTLGTNNVWPDVSLPDYKN 239
 Qy 227 IF---KSNGFPHGISPEPEDMETLEKFSVDHPVAFNFMKGLKKNPDRLTCSQLLES 283
 Db 240 TFPKWKSG-----NLASTVKNLDKNGIDILTKMLIYDPPKRSARQAMTH 284
 Qy 284 SYFDSFOEAQI 294
 Db 285 PYFDDLDKSTL 295

RESULT 8
 S22440
 Protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice
 C:Species: Oryza sativa (rice)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S22440
 R:Hashimoto, J.; Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzuka, I.; Utsugi, M. Gen. Genet. 233, 10-16, 1992
 A:Title: Isolation and characterization of cDNA clones encoding cdc2 homologues from Ory
 A:Reference number: S22440; MUID:92293101; PMID:1376401
 A:Accession: S22440
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-294 <HAS>
 A:CROSS-references: UNIPROT:P29618; EMBL:X60374; NID:G20342; PIDN:CAA42922.1; PID:G20343
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
 F:2-256/Domain: protein kinase homology <KIN>
 F:10-18/Region: protein kinase ATP-binding motif
 F:33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 34.2%; Score 568.5; DB 2; Length 294;
 Best Local Similarity 37.6%; Pred. No. 7e-20;
 Matches 117; Conservative 67; Mismatches 92; Indels 35; Gaps 9;
 Qy 1 MEKYEKLAKTGGSGVGVFKCRNKTSGOVAVKFESEDDPVVKIALREIMLKQLKH 60
 Db 1 MEQYEKEKIGEGTVGVYRARDKVTNETIALKIRLEQDEGVPTAIREISLLKEMH 60
 Qy 61 PNLVNLIEVFRKRMHLVFEYCDHTLLN-----ELERNPVGADGVKSVLMQTLQAL 114
 Db 61 GNIVRLHDVHSEKRIYLVFEYLDLKLKFMDSCEPEAKNPT-----LIKSYLVQILRGV 115
 Qy 115 NFCHINCHIRDIKPNILITKQ-GIIKICDFGPAQIL-IPGDAYTDYVATRYRAPELL 172
 Db 116 AYCHSHRVLRDLKPNLLDRIINALKIADFGRLAFGVPTFTHEVVTLMYRAPEIL 175
 Qy 173 VGDYQSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIPRHOSIFKSN 232
 Db 176 LGSRYQYTPVDMWSVGCIFAEVWQKELFPDSEIDELFKIFVLG--TFNEQS----- 227
 Qy 233 FFHGI-SIP-----EPEDMETLEKFSVDHPVAFNFMKGLKKNPDRLTCSQLLE 282
 Db 228 -WPGVSLPDYKAPFKWQAQDLATI---VPTLDPAGLDLSKMLRYEPNKRITARQALE 283
 Qy 283 SSYFDSFOEAQ 293
 Db 284 HEYFKDLEMQV 294

RESULT 9
 A41227
 protein kinase (EC 2.7.1.37) cdk2 - human
 N:Alternate names: Egl homolog; protein kinase p34
 C:Species: Homo sapiens (man)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C:Accession: A41227; S17873; S16520

R:Ninomiya-Tsujii, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
 A:Title: Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a t
 A:Reference number: A41227; MUID:92020980; PMID:1717994
 A:Accession: A41227
 A:Molecule type: mRNA
 A:Residues: 1-298 <NIN>
 A:CROSS-references: UNIPROT:P24941; GB:M68520; NID:G180177; PIDN:AAA35667.1; PID:G180178
 R:Tsal, L.H.; Harlow, E.; Meyerson, M.
 Nature 353, 174-177, 1991
 A:Title: Isolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-
 A:Reference number: S17873; MUID:91367262; PMID:1653904
 A:Accession: S17873
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <TSA>
 A:CROSS-references: GB:X62071; NID:G312802; PIDN:CAA43985.1; PID:G312803
 R:Elledge, S.J.; Spottswood, M.R.
 EMBO J. 10, 2853-2859, 1991
 A:Title: A new human p34 protein kinase, CDK2, identified by complementation of a cdc28 n
 A:Reference number: S16520; MUID:91330891; PMID:1714386
 A:Accession: S16520
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-176, 'S', 178-298 <ELL>
 A:CROSS-references: EMBL:X61622; NID:G29848; PIDN:CAA43807.1; PID:G29849
 C:Genetics:
 A:Gene: GDB:CDK2
 A:CROSS-references: GDB:128984; OMIM:116953
 A:Map position: 12q13-12q13
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine/
 F:2-255/Domain: protein kinase homology <KIN>
 F:10-18/Region: protein kinase ATP-binding motif
 F:14,160/Binding site: phosphate (Thr) (covalent) #status predicted
 F:15/Binding site: phosphate (Tyr) (covalent) #status predicted
 F:33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 34.1%; Score 567; DB 2; Length 298;
 Best Local Similarity 40.0%; Pred. No. 8.3e-20;
 Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6;
 Qy 1 MEKYEKLAKTGGSGVGVFKCRNKTSGOVAVKFESEDDPVVKIALREIMLKQLKH 60
 Db 1 MENFQKEKIGEGTVGVYKARKNLGTGEVVALKIRLDTETEGVPSTAIRSILLKELNH 60
 Qy 61 PNLVNLIEVFRKRMHLVFEYCDHTLLNELRN-NGVADGVKSVLMQTLQALNFCI 119
 Db 61 PNIVKLLDVIHTENKLYLVFEFLHQLDKKFMDSALGTGIPLPLKSYLVFQLQLGATFCHS 120
 Qy 120 HNCIHRDIKPNILITKQIIGIICDFGPAQIL-IPGDAYTDYVATRYRAPELLVGDYQ 178
 Db 121 HRVLRDLKPNLLDRIINALKIADFGRLAFGVPTFTHEVVTLMYRAPEILLGCKY 180
 Qy 179 GSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIPRHOSIFKSNFFHGI- 237
 Db 181 STAVDINSGLGICFAEVMYTRALFPDSEIDQLFRIFTLGT-----PDEVVWFQVT 231
 Qy 238 SIPE--PEDMETLEKFSVDHPV-----ALNFMKGLKKNPDRLTCSQLLESYF 286
 Db 232 SMPDKSFPKWARQDFSKVVPPLDEDRSLLSQMLHYDENKRIKSAKAAHAHPFF 286

RESULT 10
 A37871
 protein kinase (EC 2.7.1.37) cdk2 - African clawed frog
 N:Alternate names: cell division control protein CDC2 homolog Egl
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
 C:Accession: A37871; S15866; I51662; S14410
 R:Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camonis, J.; Macn
 Proc. Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991
 A:Title: Cloning by differential screening of a Xenopus cDNA coding for a protein highly

A;Reference number: A37871; MUID:91126051; PMID:1704128

A;Accession: A37871

A;Molecule type: mRNA

A;Residues: 1-297 <PAR>

A;Cross-references: UNIPROT:P23437; UNIPROT:Q9PSU0; GB:X14227

R;le Guellac, R.

submitted to the EMBL Data Library, January 1989

A;Reference number: S15866

A;Accession: S15866

A;Molecule type: mRNA

A;Residues: 1-92,'R',94-297 <LEA>

A;Cross-references: EMBL:X14227; NID:g64665; PIDN:CAA32443.1; PID:g64666

R;Olive, M.; Theze, N.; Philippe, M.; Le Pennec, J.P.; Leirivay, H.

Gene 151, 81-88, 1994

A;Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in oocytes

A;Reference number: S151662; MUID:95129896; PMID:7828909

A;Accession: S151662

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-39 <OLI>

A;Cross-references: EMBL:U07979; NID:g473584; PIDN:AAA82123.1; PID:g473585

C;Genetics:

A;Gene: cdk2

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase

F;2-255/Domain: protein kinase homology <KIN>

F;10-18/Region: protein kinase ATP-binding motif

F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 34.0%; Score 565.5; DB 2; Length 297;

Best Local Similarity 37.8%; Pred. No. 9.7e-20;

Matches 116; Conservative 65; Mismatches 85; Indels 41; Gaps 6;

Qy 1 MEKYEKLAKTGEQSGYGVFKCRNKTSCQVAVKVFSEDDPVVKYKIALREIRMLKQLKH 60

Db 1 MENFQKEKIGEGYGVYKARNRETGEIVALKIRLDTETEGVPSAIREISLLKELNH 60

Qy 61 PNLVNLLEVFRRKRKMHLEVEYCDHTLLNELE-RNPNGVADGVTKSVLWOTLQALNFCI 119

Db 61 PNLVNLLEVFRRKRKMHLEVEYCDHTLLNELE-RNPNGVADGVTKSVLWOTLQALNFCI 119

Qy 120 HNCITHRDKPENILITKQGIKICDFGAQIL-IPGDAYTDYVATRYRAPELLVGDQY 178

Db 121 HRVLRDLKPNQLLIDRTNSLKLADFLARAFGIPVTFTHVVTLYRAPELLVGSHT 180

Qy 179 GSSVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLG-----KLIPRHQSI 228

Db 181 STAVDIWSLGCIFAEITRRALFGDSEIDQLFRIFTLGTPDEVSNPGVTTPDYKSTP 240

Qy 229 KSNQGFPHGISIPEPEDEMETLEEKFSVHPVALNFMKGLKMPDRDLTCSQLLESSYFDS 288

Db 241 P-----KWIRQDPSKVVP-----PLDEGRDLAQLQ---YDS 271

Qy 289 FQEAQIK 295

Db 272 NKRTSAK 278

RESULT 11

S23095

protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana

N;Alternate names: cdc2 protein homology; CDC2a protein; cell division control protein 2

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S23095; A48984; J01337; JQ0967; S18202

R;Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.

FEBS Lett. 304, 73-77, 1992

A;Title: Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a

A;Reference number: S23095; MUID:92316202; PMID:1618302

A;Accession: S23095

A;Molecule type: DNA

A;Residues: 1-294 <INA>

A;Cross-references: UNIPROT:P24100; EMBL:D10850; NID:g217848; PIDN:BAA01623.1; PID:g2178

R;Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.

Biochem. Soc. Trans. 20, 80-84, 1992

A;Title: Control of cell division in plants.

A;Reference number: A48984; MUID:92339744; PMID:1634002

A;Accession: A48984

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-294 <INZ>

A;Experimental source: flower

A;Note: sequence extracted from NCBI backbone (NCBIP:109461)

R;Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.

Gene 105, 159-165, 1991

A;Title: Identification of two cell-cycle-controlling cdc2 gene homologs in Arabidopsis

A;Reference number: JQ1337; MUID:92039027; PMID:1937013

A;Accession: JQ1337

A;Molecule type: mRNA

A;Residues: 1-294 <HIF>

A;Cross-references: EMBL:X57839; NID:g16218; PIDN:CAA40971.1; PID:g16219

R;Ferreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze, D.

Plant Cell 3, 531-540, 1991

A;Title: The Arabidopsis functional homolog of the p34cdc2 protein kinase.

A;Reference number: JQ0967; MUID:93005715; PMID:1840925

A;Accession: JQ0967

A;Molecule type: mRNA

A;Residues: 1-294 <FER>

A;Cross-references: GB:S45387; NID:g257373; PIDN:AAB23643.1; PID:g257374

A;Experimental source: flower

C;Comment: The protein is a key component of the eukaryotic cell cycle.

C;Genetics:

A;Gene: cdc2

A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3

C;Function:

A;Description: phosphotransferase; protein kinase; required for G1 to S-phase transition;

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase

F;2-256/Domain: protein kinase homology <KIN>

F;10-18/Region: protein kinase ATP-binding motif

F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.8%; Score 561.5; DB 2; Length 294;

Best Local Similarity 37.1%; Pred. No. 1.5e-19;

Matches 111; Conservative 70; Mismatches 93; Indels 25; Gaps 6;

Qy 1 MEKYEKLAKTGEQSGYGVFKCRNKTSCQVAVKVFSEDDPVVKYKIALREIRMLKQLKH 60

Db 1 MDQYKEKIGEGYGVYKARNRETGEIVALKIRLDTETEGVPSAIREISLLKEMQH 60

Qy 61 PNLVNLLEVFRRKRKMHLEVEYCDHTLLNELE-RNPNGVAD-GVTKSVLWOTLQALNFCI 119

Db 61 SNIVKQDVVHSBKRLVLFVEYLDLDLKKHMDSTPDFSKLHMKTLYQLRGIAVCHS 120

Qy 120 HNCITHRDKPENILITKQ-GIHKICDFGAQIL-IPGDAYTDYVATRYRAPELLVGDQY 177

Db 121 HRVLRDLKPNQLLIDRTNSLKLADFLARAFGIPVTFTHVVTLYRAPELLVGSHT 180

Qy 178 YGSSVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLG-----KLIPRHQSI 227

Db 181 YSTPVDIWSVGCIFAEMISQKPLFGDSEIDQLFKIFRIMGTPYEDTWGVTSLPDYKSA 240

Qy 228 FKSNGFPHGISIPEPEDEMETLEEKFSVHPVALNFMKGLKMPDRDLTCSQLLESSYF 286

Db 241 FPX-----WKPTDLETF---VPLNDPGVDLLSKMLMDPTKKNARAALAEHYF 287

RESULT 12

A44349

protein kinase (EC 2.7.1.37) cdc2-A [similarity] - African clawed frog

N;Alternate names: maturation-promoting factor p34cdc2 chain A

C;Species: Xenopus laevis (African clawed frog)

C;Date: 05-May-2000 #sequence revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: A44349

R;Pickham, K.M.; Meyer, A.N.; Li, J.; Donoghue, D.J.

Mol. Cell. Biol. 12, 3192-3203, 1992

A:Title: Requirement of mos(Xe) protein kinase for meiotic maturation of Xenopus oocytes
A:Reference number: A44349; MUID:92318937; PMID:137775

A:Accession: A44349
A:Molecule type: mRNA
A:Residues: 1-302 <PIC>
A:Cross-references: UNIPROT:P35567; GB:M60680; NID:g214022; PIDN:AAA63561.1; PID:g214023
A:Experimental source: oocytes
A:Note: sequence extracted from NCBI backbone (NCBI:107682, NCBI:P:107683)
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F:2-256/Domain: protein kinase homology <KIN>
F:10-18/Region: protein kinase ATP-binding motif
F:33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.6%; Score 559; DB 1; Length 302;
Best Local Similarity 36.7%; Pred. No. 2e-19;
Matches 117; Conservative 68; Mismatches 102; Indels 32; Gaps 6;

QY 1 MEKYEKLAKTGESYGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MDEYTKIEKIGEGTYGVVYKGRHATGQVAVKIRLENEREGVPSTAIRLSLKELOH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPG--VADGVKSVLMOTLQALNFC 118
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPG--VADGVKSVLMOTLQALNFC 118
QY 119 INNCIHRDIPENILITKQGIKIICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDQ 177
DB 121 SRRLVRLDKLPQNLLIDSGVKIKLADFGARAFGIPRVYTHEVVTLMYRAPELLVGSVR 180
QY 178 YGSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGKLIPIRHOSIFKSNFFHG 237
DB 181 YSTPVDVWSIGTIFAEIATKPLFHGSDSEIDQLFRFALG--TPNNE----- 226
QY 238 SIPEDEMTELEKFSFSDVHPVA-----LNFMKGCCKMNPDDRLTCSQLLESSY 285
DB 227 VMPVESLQDYKNTFPKPKGSLASHVKNLDEGLDLSKMLVYDPAKRIKSGMALKHP 286
QY 286 FDSFOEAQIKRKARNEGRN 304
DB 287 FDDLKSSSL---PDNQIRN 302

RESULT 13
S24913
protein kinase (EC 2.7.1.37) cdc2 [similarity] - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: S24913
R:Kanaoka, Y.; Nojima, H.; Okayama, H.
A:Description: Nucleotide sequences of cDNAs encoding rat cdc2 + and cyclin 2.
A:Reference number: S20658

A:Accession: S24913
A:Molecule type: mRNA
A:Residues: 1-297 <KAN>
A:Cross-references: UNIPROT:P39951; EMBL:X60767; NID:g57533; PIDN:CAA43177.1; PID:g57534
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F:2-256/Domain: protein kinase homology <KIN>
F:10-18/Region: protein kinase ATP-binding motif
F:33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.5%; Score 557; DB 1; Length 297;
Best Local Similarity 39.1%; Pred. No. 2.4e-19;
Matches 122; Conservative 63; Mismatches 95; Indels 32; Gaps 8;

QY 1 MEKYEKLAKTGESYGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 59
DB 1 MEDYTKIEKIGEGTYGVVYKGRHATGQVAVKIRLENEREGVPSTAIRLSLKELOH 59
QY 60 HPNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPG--VADGVKSVLMOTLQALNFC 117

DB 60 HPNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPG--VADGVKSVLMOTLQALNFC 119
QY 118 HHCNCIHRDIPENILITKQGIKIICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 176
DB 120 HSRLVRLDKLPQNLLIDSGVKIKLADFGARAFGIPRVYTHEVVTLMYRAPELLVGS 179
QY 177 YGSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGKLIPIRHOSIFKSNFFHG 236
DB 180 RYSTPVDVWSIGTIFAEIATKPLFHGSDSEIDQLFRFALG--TPNNE----- 226
QY 237 SIPEDEMTELEKFSFSDVHPVA-----LNFMKGCCKMNPDDRLTCSQLLESS 284
DB 227 VMPVESLQDYKNTFPKPKGSLASHVKNLDEGLDLSKMLVYDPAKRIKSGMALKHP 285
QY 285 YFDSFOEAQIKRK 296
DB 286 YFDDL-DNQIKK 296

RESULT 14
T49271

CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A - Arabidopsis thaliana
N:Alternate names: protein T2J18.20
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Accession: T49271
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25021

A:Accession: T49271
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-294 <RIE>
A:Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T2J18.20
A:Experimental source: cultivar Columbia; BAC clone T2J18
C:Genetics:
A:Gene: ATSP:T2J18.20
A:Map position: 3
A:Introns: 3/3; 67/3; 105/3; 163/3; 218/2; 247/3; 265/3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 33.5%; Score 556.5; DB 2; Length 294;
Best Local Similarity 36.8%; Pred. No. 2.5e-19;
Matches 110; Conservative 70; Mismatches 94; Indels 25; Gaps 6;

QY 1 MEKYEKLAKTGESYGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MDQYEKVEKIGEGTYGVVYKARDKVTNETIALKKIRLEQDEGVSTAIRSILKEMQH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVAD-GVIKSVLMOTLQALNFC 119
DB 61 SNIVKYDDVHSEKRLVFEYLDLKKHMDSPDFSKLHMLTKLYLQIRGIAYCHS 120
QY 120 HNCIHRDIPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 177
DB 121 HSRLVRLDKLPQNLLIDRTNSKLADFGARAFGIPRVYTHEVVTLMYRAPELLVGS 180
QY 178 YGSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLG-----KLIPRHOSI 227
DB 181 YSTPVDVWSIGTIFAEIATKPLFHGSDSEIDQLFRFALG--TPNNE----- 240
QY 228 FKSNGFFHGSIPEDEMTELEKFSFSDVHPVAFNFMKGCCKMNPDDRLTCSQLLESSY 286
DB 241 FPK-----WKPTDLETF---VPLNDPDGVDLLSKMLMDPTKINARAALHEHYF 287

RESULT 15

A29539
protein kinase (EC 2.7.1.37) cdc2 - human
N:Alternate names: cell division control protein 2 (CDC2)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: A29539

R:Lee, M.G.; Nurse, P.
 Nature 327, 31-35, 1987
 A;Title: Complementation used to clone a human homologue of the fission yeast cell cycle
 A;Reference number: A29539; MUID:87201915; PMID:3553962
 A;Accession: A29539
 A;Molecule type: mRNA
 A;Residues: 1-297 <LEE>
 A;Cross-references: UNIPROT:P06493; GB:X05360; NID:g29838; PIDN:CAA28963.1; PID:g29839
 C;Genetics:
 A;Gene: GDB: CDC2
 A;Cross-references: GDB:119052; OMIM:116940
 A;Map position: 10q21.1-10q21.1
 C;Superfamily: kinase-related transforming protein; protein kinase homology
 C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
 F;2-256/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;14,161/Binding site: phosphate (Thr) (covalent) #status predicted
 F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
 F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.5%; Score 556; DB 2; Length 297;
 Best Local Similarity 39.4%; Pred. No. 2.7e-19;
 Matches 123; Conservative 61; Mismatches 96; Indels 32; Gaps 8;

Qy	1	MEKYEKLAKTCEGSYGVVFKCRNKTSGQVAVKKE-VESEDDPVVKIALREIRMLKQLK	59
Db	1	MEDYTKIEKIGEGTYGVVYKGRHKTTGQVAMKKIRLESEEEG-VPSTAIRIETSLKREL	59
Qy	60	HPNLVNLIIEVRRKRKMHVPEYCDHTLLNELERNPNG--VADGVIKSVLMQTLQALNFC	117
Db	60	HPNIVSLQDVLQMDSRLYLIFEFLSMDLKKYLDISIPFGQYWDSSLVKSXYLIQLQGIIVFC	119
Qy	118	HIHNCIHRDIKENILITKQGIKICDFGAQIL-IPGDAYTDYVATRWYRAPELLVGD	176
Db	120	HSRRVLHRLKPNLLIDDKGTIKLADFGLARAFGIPRVVYTHEVVTWYRSPEVLIGSA	179
Qy	177	QYGSVDIWAIGCVFAELLTCQPLWPGKSDVDQYLIIRTLGKLI PRHQIFKSNGFHG	236
Db	180	RYSTPVDIWSIGTIFAEELATKKPLFHGDSEIDQLFRIFRALG--TPNNE-----	226
Qy	237	ISIPEPEDEMETLEKFSDFVHPVA-----LNFMKGLKMNPPDRITCSQLES	284
Db	227	-VMFEVESLQDYKNTFPKWFPGSLASHVKNLDEGLDLKMLIYDPAKRISGKMLNHP	285
Qy	285	YFDSFQEAQIKR	296
Db	286	YFNDL-DNQIKK	296

Search completed: April 22, 2005, 06:51:40
 Job time : 26.6949 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:29:40 ; Search time 82.7946 Seconds
(without alignments)
1948.255 Million cell updates/sec

Title: US-10-766-691-12
Perfect score: 1562
Sequence: 1 MEKYEKLAKTGGSGYGVFK.....RKARNEGRRRROQVLPKLS 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1209.5	72.8	350	Q6AXJ9	Q6axj9 brachydanio
2	1206	72.6	352	Q8CEQ0	Q8ceq0 mus musculus
3	1188.5	71.5	358	Q6QUA0	Q6qua0 homo sapien
4	1184	71.2	352	Q66HE7	Q66he7 rattus norv
5	1183.5	71.2	358	1 KIA_HUMAN	Q00532 homo sapien
6	1035.5	62.3	367	Q7QBG7	Q7qbg7 anopheles g
7	1027.5	61.8	353	Q9U2H1	Q9u2h1 caenorhabdi
8	1027.5	61.8	392	Q9VMN3	Q9vmn3 drosophila
9	967.5	58.2	566	Q9TTK0	Q9ttk0 oryctolagus
10	958	57.6	385	Q675R9	Q675r9 oikopleura
11	941.5	56.6	493	Q9QY12	Q9qy12 mus musculus
12	930.5	56.0	564	Q9QY12	Q9qy12 mus musculus
13	930.5	56.0	568	Q9QY11	Q9qy11 mus musculus
14	928	55.8	329	Q9QY11	Q9qy11 mus musculus
15	924	55.6	320	Q6GMD6	Q6gmd6 xenopus lae
16	919.5	55.3	651	Q6TXH3	Q6txh3 rattus norv
17	784.5	47.2	455	Q9P114	Q9p114 homo sapien
18	784.5	47.2	592	Q9IVW4	Q9ivw4 homo sapien
19	781	47.0	657	Q9BMG2	Q9bm2 trypanosoma
20	770	46.3	353	Q8K134	Q8k134 mus musculus
21	769.5	46.3	1106	Q9GRT9	Q9grt9 leishmania
22	767.5	46.2	457	Q8BKZ2	Q8bkz2 mus musculus
23	764.5	46.0	585	Q9BLA9	Q9bla9 mus musculus
24	763.5	45.9	457	Q9JMO2	Q9jmo2 rattus norv
25	763.5	45.9	595	Q9JMO1	Q9jmo1 rattus norv
26	759.5	45.7	505	Q8BLF2	Q8blf2 mus musculus
27	720.5	43.4	783	Q8BWL8	Q8bwl8 mus musculus
28	720.5	43.4	831	Q8LYC7	Q8lyc7 homo sapien
29	720.5	43.4	1030	1 STK9_HUMAN	Q76039 homo sapien
30	708	42.6	993	2 Q8WXQ5	Q8wxq5 homo sapien
31	702.5	42.3	578	2 Q8BVE0	Q8bve0 mus musculus

32	644	38.7	1104	2	Q9W6R6	Q9w6r6 fugu rubrip
33	581.5	35.0	289	2	Q7RM49	Q7rm49 plasmodium
34	581	35.0	305	1	CDK3_HUMAN	Q00526 homo sapien
35	579.5	34.9	294	2	Q9ZRI1	Q9zri1 triticum ae
36	574.5	34.6	292	1	CC2H_DICDI	P34117 dictyosteli
37	571.5	34.4	297	1	CDK2_XENLA	P23437 xenopus lae
38	570.5	34.3	297	2	Q66IH7	Q66ih7 xenopus tro
39	570.5	34.3	302	1	CDK2_CARAU	P51958 carassius a
40	570.5	34.3	302	2	Q7T3L7	Q7t3l7 brachydanio
41	568.5	34.2	294	1	CC21_ORYSA	P29618 oryza sativ
42	567.5	34.1	303	1	CDK2_ORYJA	P49ga2 oryzias jav
43	567	34.1	298	1	CDK2_HUMAN	P24941 homo sapien
44	566.5	34.1	294	1	CDK2_MAIZE	P23111 zea mays (m
45	564	33.9	288	2	Q9XZD6	Q9xzd6 plasmodium

ALIGNMENTS

RESULT 1
Q6AXJ9 ID Q6AXJ9 PRELIMINARY; PRT; 350 AA.
AC Q6AXJ9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Zgc:101002 protein.
GN Name=zgc:101002;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Singapore local strain; TISSUE=Embryo;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek J., Schmutz J., Schmutz J., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079506; AAH79506.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001109; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser thr.pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.

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DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR NCBI; SM00219; TTKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 350 AA; 40810 MW; 9B04440EE0E38BE1 CRC64;

Query Match 72.8%; Score 1209.5; DB 2; Length 350;
Best Local Similarity 69.9%; Pred. No. 1.5e-77;
Matches 220; Conservative 47; Mismatches 45; Indels 3; Gaps 2;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
QY 61 PNLVNLIEVFRKRKRLHVFYCDHTLNLERNPNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 61 PNLVNLMEVFRKRKRLHVFYCDHTLNLERNPNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 121 NCIHREDIKPENLITKQGIKICDFGFAQILI-PCDAVTDVYATWYRAPPELLVGD 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 179
QY 121 NCIHREDVAPENLITKHQVILKCDGPARILTGPCDYDTCVATRWYRAPPELLVGD 180
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 180
QY 180 SSVDIWAIGCVPAELLTGQLPWPKSDVDOLYLIIRTLGKLIPRHQSIFKSNPFHGISI 239
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 239
QY 181 PPVDVWAVGCVFAELLGAPLWPKSDVDQLYLIRKTLGELIPRHQVFSNQFSGVCV 240
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 240
QY 240 PEPDEMETLEKFSVDVHPALNFMKGLKMPDDRLTCSQLLESYFDSFQF--AQIKRK 297
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 297
QY 241 PEPQMEPLELKYPNLSYOALSMLKGLRMDPAERLSCEQLLEQPYFDSLRESESV 300
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 300
QY 298 ARNEGRNRRRQQLVP 312
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 312
QY 301 LDRKKTKTQPRKHL 315
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 315

RESULT 2
ID Q8CEQ0 PRELIMINARY; PRT; 352 AA.
AC Q8CEQ0;
DC 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933411017 product:cyclin-dependent kinase-like 1
DE (CDC2-related kinase), full insert sequence.
GN Name=Cdkli;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK016781; BAC25497.1; -.
DR MGD; MGI:1918341; Cdkli.
DR HSSP; Q00535; 1H4L.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser thr pkinase.
DR InterPro; IPR008271; Ser thr pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
DR ATP-binding; Cyclin; Kinase; Transferase.
SQ SEQUENCE 352 AA; 41023 MW; 6E9F56C8080F35E0 CRC64;

Query Match 72.6%; Score 1206; DB 2; Length 352;
Best Local Similarity 68.9%; Pred. No. 2.7e-77;
Matches 222; Conservative 42; Mismatches 48; Indels 10; Gaps 3;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
QY 1 MEKYEKIKIGSGYGVVFKCRNRTGQIVAKRFELEDDEDPVVKKIALREIRMLKQLKH 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
QY 61 PNLVNLIEVFRKRKRLHVFYCDHTLNLERNPNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 61 PNLVNLMEVFRKRKRLHVFYCDHTLNLERNPNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 121 NCIHREDIKPENLITKQGIKICDFGFAQILI-PCDAVTDVYATWYRAPPELLVGD 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 179

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Db 121 NCIRDVKPENILITKQSAIKLCDFGPARLITGSDYTDVATWTRSPPELLVGDITQYG 180
Qy 180 SSVDIWAIGCVFABELLTGQPLWPKGSDVDQLYLIRTLGKLIPIRHQSIFKSNFGFHGISI 239
Db 181 PPVDVWAIGCVFABELLGVLWPKGSDVDQLYLIRTLGDLIPRHQVFSNQVFSGVKI 240
Qy 240 PEPEDMETLEKFSVDHPVAFNMFKGCLKNPDDRLTCSQLLESSYFDSFQEA-----QI 294
Db 241 PDPEDMETLEKFPNISYALGFLKGLCHMDPAERLTCEQLLQHPYFDSREVGEGLTROH 300
Qy 295 KRKARNEGRNRQ---QVLP 312
Db 301 DKPARKTLRQSRKLTGLQYLP 322

RESULT 3
Q6QUAO PRELIMINARY; PRT; 358 AA.
AC Q6QUAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase-like 1 (CDC2-related kinase).
GN Name=CDK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY525548; AAS00095.1; --
DR HSP; P24941; 1838.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Cyclin; Kinase; Transferase.
SQ SEQUENCE 358 AA; 41833 MW; 823E432BF84B77C6 CRC64;

Query Match 71.5%; Score 1188.5; DB 2; Length 358;
Best Local Similarity 70.5%; Pred. No. 4.8e-76;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFKFVSEDDPVVKYKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDGTQVAIKKFKFSEDDPVVKYKIALREIRMLKQLKH 61
Qy 61 PNLVNLLEVRKRKRLHVPYCDHTLLNELERNPNGVADGVKSVLWOTLQALNFCIH 120
Db 62 PNLVNLLEVRKRKRLHVPYCDHTLVHLEDYRQGVPEHLVKSITWTLQAVNFCCHK 121
Qy 121 NCIRDVKPENILITKQGIKICDFGFAQLI--PGDAYTVATWTRAPPELLVGDITQYG 179
Db 122 NCIRDVKPENILITKHSVVKLCDFGPARLITGSDYTDVATWTRSPPELLVGDITQYG 181

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Qy 180 SSVDIWAIGCVFABELLTGQPLWPKGSDVDQLYLIRTLGKLIPIRHQSIFKSNFGFHGISI 239
Db 182 PPVDVWAIGCVFABELLGVLWPKGSDVDQLYLIRTLGDLIPRHQVFSNQVFSGVKI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMFKGCLKNPDDRLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PDPEDMEPLEKFPNISYPALGFLKGLCHMDPTELTCEQLLHHPYFENIREIEDLAKEH 301
Qy 300 NE 301
Db 302 NK 303

RESULT 4
Q66HE7 PRELIMINARY; PRT; 352 AA.
AC Q66HE7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081896; AAH81896.1; --
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 40899 MW; DB9CDF5464B66E24 CRC64;

Query Match 71.2%; Score 1184; DB 2; Length 352;
Best Local Similarity 69.0%; Pred. No. 9.7e-76;
Matches 214; Conservative 45; Mismatches 49; Indels 2; Gaps 2;

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QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKVFESDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYEKIGKGGSGYGVVFKCRNKTSGOVAVKVFESDDPVVKKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRRLHLVFEYCDHTLLNELRNPNMGVADGVKSVLWOTLOALNFCCHI 120
Db 61 PNLVNLIEVFRKRRLHLVFEYCDHTLLNELRNPNMGVADGVKSVLWOTLOALNFCCHI 120
QY 121 NCIHRLDKPENILITKQGIITKIDFGFAQILI-PGDAYTDDYVATRYRAPELLVGTQYG 179
Db 121 NCIHRLDKPENILITKHSVILKIDFGFAQILI-PGDAYTDDYVATRYRAPELLVGTQYG 179
QY 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQVLYLIIRTLGKLIIRHOSIFKSNFGFHGIST 239
Db 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQVLYLIIRTLGKLIIRHOSIFKSNFGFHGIST 239
QY 240 PEPEDMETLEKESDVHPVVALNFMKGLKQNPDPDLRTCSQLLESSYFDSFQF-AQIKRKA 298
Db 240 PEPEDMETLEKESDVHPVVALNFMKGLKQNPDPDLRTCSQLLESSYFDSFQF-AQIKRKA 298
QY 299 RNEGRNRRRQ 308
Db 301 DKPTRKTLRQ 310

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RESULT 5

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KXIA_HUMAN
ID KXIA_HUMAN STANDARD; PRT; 358 AA.
AC Q00532;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase KXIALRE (EC 2.7.1.37) (Cyclin-
DE dependent kinase-like 1).
GN Name=CDKL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=92347325; PubMed=1639063;
RA Meyerson M., Enders G.H., Wu C.-L., Su L.-K., Gorka C., Nelson C.,
RA Harlow E., Tsai L.-H.;
RT "A family of human cdc2-related protein kinases.";
RL EMBO J. 11:2909-2917(1992).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC CDC2/CDKX subfamily.

```

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```

DR EMBL; X66358; CAA47002.1; -.
DR EMBL; X66359; CAA47002.1; JOINED.
DR PIR; S23383; S23383.
DR HSPF; P24941; LH00.
DR Genew; HGNC:1781; CDKL1.
DR MIM; 603441; -.
DR GO; GO:0004693; F:cyclin-dependent protein kinase activity; TAS.
DR GO; GO:000468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR008719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.

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```

DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 5 288 Protein kinase.
FT NP_BIND 11 19 ATP (By similarity).
FT BINDING 34 34 ATP (By similarity).
FT ACT_SITE 127 127 Proton acceptor (By similarity).
SQ SEQUENCE 358 AA; 41834 MW; 88344321F24B77C6 CRC64;

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Query Match 71.2%; Score 1183.5; DB 1; Length 358;
Best Local Similarity 71.8%; Pred. No. 1.1e-75;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKVFESDDPVVKKIALREIRMLKOLKH 60
Db 2 MEKYEKIGKGGSGYGVVFKCRNKTSGOVAVKVFESDDPVVKKIALREIRMLKOLKH 61
QY 61 PNLVNLIEVFRKRRLHLVFEYCDHTLLNELRNPNMGVADGVKSVLWOTLOALNFCCHI 120
Db 62 PNLVNLIEVFRKRRLHLVFEYCDHTLLNELRNPNMGVADGVKSVLWOTLOALNFCCHI 121
QY 121 NCIHRLDKPENILITKQGIITKIDFGFAQILI-PGDAYTDDYVATRYRAPELLVGTQYG 179
Db 122 NCIHRLDKPENILITKHSVILKIDFGFAQILI-PGDAYTDDYVATRYRAPELLVGTQYG 181
QY 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQVLYLIIRTLGKLIIRHOSIFKSNFGFHGIST 239
Db 182 PVDVWAIGCVFAELLTGQPLWPKSDVDQVLYLIIRTLGKLIIRHOSIFKSNFGFHGIST 241
QY 240 PEPEDMETLEKESDVHPVVALNFMKGLKQNPDPDLRTCSQLLESSYFDSFQF-AQ 293
Db 242 PEPEDMETLEKESDVHPVVALNFMKGLKQNPDPDLRTCSQLLESSYFDSFQF-AQ 295

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RESULT 6

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Q7QBG7
ID Q7QBG7 PRELIMINARY; PRT; 367 AA.
AC Q7QBG7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP3044.
GN Name=agCG5557; ORFNames=ENSANGG00000012213;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008879; EAA08474.1; -.
DR HSSP; P24941; 101Q.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.

```

DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW	ATP-binding; Hypothetical protein; Kinase; Transferase.
SQ	SEQUENCE 353 AA; 40665 MW; 7E3226D9849CAC9 CRC64;

Query Match	61.8%;	Score 1027.5;	DB 2;	Length 353;
Best Local Similarity	58.8%;	Pred. No. 1.le-64;		
Matches 187;	Conservative 59;	Mismatches 63;	Indels 9;	Gaps 2

Qy	1	MEKYEKLAKTGGEGYGVVFKCRNKTSGQVAVKFVESEDDPVVKIARLRIRMLKQLKH	60
Db	1	MDKYDLRLSKLGEGSYGVVYCKNRDTGQIVAKKFVEDTDPHIKIARLRIRMLKQLKH	60
Qy	61	PNLVNLLEVFERRKKMHLVPFYCDHTLLNELRNPNGVADGYKSVLQTLQALNFCHTH	120
Db	61	QNVLGLLEVFKRNKRKLHVLFCLDRTVLHELEKHPGVNDLELIKIIQLLEALAFCHSH	120
Qy	121	NCIHRDIKENILITKGIIKICDFGAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS	180
Db	121	KCIHRDVKPENIFLTRNDQVKLGDFGARINTTEMTYDYVATRWYSPELLVGDVQYGP	180
Qy	181	SVDIWAIGCVFAELLITCQPLPWGSDVDOLYLITRTGLKLPKHOSIPKSNFFHGISIP	240
Db	181	PVDIWAIGCVYAELLTGEALWPGRSIDIQLXHKRTGLEFLPRHISISFTNQFFELSLP	240
Qy	241	EPEDMETLEBKFSVDHPVALNFMKGLKNPPDDLTCQSLESSEYDFSQEAQIRKRN	300
Db	241	EPEHLEPLPSKLWNASSAQDLDFLOCKCEMSDPRFSCSELMLHGIFSNN-----ILLRQD	296
Qy	301	EG-----NRRRRQQVLPFL	313
Db	297	ESTPTGLTSKRSNPYLPL	314

RESULT #	Q9VMN3	PRELIMINARY;	PRT;	392 AA.
ID	Q9VMN3			
AC	Q9VMN3;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	CG7236-PA.			
GN	ORFNames=CG7236;			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;			
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Ananatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,			
RA	Abdel J.F., Agbayani A., An H.J., Andrews-Brannkoch C., Baldwin D.,			
RA	Balleg R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hosdin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			

Db 1 MEKYNLGVGSGVMKCNKDSGRIVAIFKFESEDDDMVKVKIAMREIKLLKQLRH 60
 Qy 61 PNLVNLIEVFRKRKMHLLVFCYDHTLLNELRNPNGVADGVKISVLWQTLQALNFCIH 120
 Db 61 ENLVNLIEVCKKRWLVYFVFDHTLDDLEFPNGLDQVQKYLFOIINGIGFCHSH 120
 Qy 121 NCIRDIKPENILITKQGIKICDGFPAQIL-IPGDYTDVATRWYRAPELLVGDYQYG 179
 Db 121 NCIRDIKPENILVSGQVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDYQYG 180
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHGISI 239
 Db 181 KAVDVAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHGISI 240
 Qy 240 PEPEDMETLEKFSVDVHPVAFNMFKGCLKNPDDRLTCSQLLESSYF--DSF-----QEA 292
 Db 241 PEIKSEPLERRYPKLSSEVLDLAKCLHVPDKRPFCAELLHDDFFQMDGFAERFSQEL 300
 Qy 293 QIK--RKARN-----EGNRRRQ 309
 Db 301 QMKVQKQARNISLSKKSQNRKKEK 324

RESULT 10

Q675R9 PRELIMINARY; PRT; 385 AA.
 AC Q675R9;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Cyclin-dependent kinase-like 1.
 GN ORFNames=006-03;
 OS Oikopleura dioica.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
 OC Oikopleuridae; Oikopleura.
 OC NCBI_TaxID=34765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15343333; DOI=10.1038/nature02709;
 RA Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,
 RA Hansen A., Flaatt M., Weissenbach J., Lehrach H., Wincker P.,
 RA Reinhardt R., Chourrout D.,
 RT "Hox cluster disintegration with persistent anteroposterior order of
 RT expression in Oikopleura dioica."
 RL Nature 431:67-71(2004).
 DR EMBL; AY449462; AAS21447.1;
 DR GO; GO:0016301; F-kinase activity; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR01245; Tyr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 385 AA; 45512 MW; 059F814421ACADAI CRC64;

Query Match 57.6%; Score 958; DB 2; Length 385;
 Best Local Similarity 57.9%; Pred. No. 1e-59;
 Matches 168; Conservative 58; Mismatches 62; Indels 2; Gaps 1;

Qy 2 EYKELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIARLREIMLKQLKHP 61
 Db 4 DKYEIKISGSGYIVKCNRETRAIVAKRIFESSEELNIIKKIAMREIMLKSLKHQ 63
 Qy 62 NLVNLIEVFRKRKMHLLVFCYDHTLLNELRNPNGVADGVKISVLWQTLQALNFCIH 121
 Db 64 NLVNLIEVYKRRKMHLLVFCYDHTLVITELSONPHGLPEQSIKRIIQQVLKGLSFCHAQ 123

Qy 122 CIHRDIKPENILITKQGIKICDGFPAQILIPGDYTDVATRWYRAPELLVGDYQYSS 181
 Db 124 CIHRDVKPENILITKQGIKICDGFPAQILIPGDYTDVATRWYRAPELLVGDYQYSS 183
 Qy 182 VDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHG--ISI 239
 Db 184 VDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHG--ISI 243
 Qy 240 PEPEDMETLEKFSVDVHPVAFNMFKGCLKNPDDRLTCSQLLESSYFDSF 289
 Db 244 TSPRVPVIEALYPAKPSHTISFLKNCLOMDPTWRLDCVELLDHAYFDY 293

RESULT 11

Q92772 PRELIMINARY; PRT; 493 AA.
 AC Q92772;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE P56 KKIAMRE protein kinase.
 GN Name=KKIAMRE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97152547; PubMed=9000130;
 RA Taglienti C.A., Wysk M., Davis R.J.;
 RT "Molecular cloning of the epidermal growth factor-stimulated protein
 RT kinase p56 KKIAMRE."
 RL Oncogene 13:2563-2574(1996).
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; U35146; AAC50918.1; --
 DR HSSP; P24941; IH00
 DR GENE; HGNC:1782; CDKL2.
 DR GO; GO:0004672; F-protein kinase activity; TAS.
 DR GO; GO:0007548; P:sex differentiation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;

Query Match 56.6%; Score 941.5; DB 2; Length 493;
 Best Local Similarity 53.1%; Pred. No. 1.9e-58;
 Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIARLREIMLKQLKH 60
 Db 1 MEKYNLGVGSGYIVKCNKRTSGQVAVKVFESDDPVVKIARLREIMLKQLRH 60
 Qy 61 PNLVNLIEVFRKRKMHLLVFCYDHTLLNELRNPNGVADGVKISVLWQTLQALNFCIH 120
 Db 61 ENLVNLIEVCKKRWLVYFVFDHTLDDLEFPNGLDQVQKYLFOIINGIGFCHSH 120
 Qy 121 NCIRDIKPENILITKQGIKICDGFPAQIL-IPGDYTDVATRWYRAPELLVGDYQYG 179
 Db 121 NCIRDIKPENILVSGQVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDYQYG 180
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHGISI 239
 Db 181 KAVDVAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHGISI 240
 Qy 240 PEPEDMETLEKFSVDVHPVAFNMFKGCLKNPDDRLTCSQLLESSYF--DSF-----QEA 292
 Db 241 PEIKEREPLERRYPKLSSEVLDLAKCLHVPDKRPFCAELLHDDFFQMDGFAERFSQEL 300

Qy 293 QIK--RKARN-----EGRNRRQ 309
 Db 301 QLKVKQDARNVSLSKSNRKK 324

RESULT 12

Q9QY12 PRELIMINARY; PRT; 564 AA.
 AC Q9QY12; 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Ser/Thr kinase KKIAMRE-gamma.
 GN Name=Cdk12; Synonyms=Kkm;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AB029066; BAA88428.1; JOINED.
 DR EMBL; AB029066; BAA88428.1; JOINED.
 DR EMBL; AB029066; BAA88428.1; JOINED.
 DR HSSP; P24941; IOIQ.
 DR MGD; MGI:1858227; Cdk12.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser thr pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 564 AA; 63640 MW; DACDEF630CC88205 CRC64;

Query Match 56.0%; Score 930.5; DB 2; Length 564;
 Best Local Similarity 53.4%; Pred. No. 1.3e-57;
 Matches 174; Conservative 66; Mismatches 69; Indels 17; Gaps 6;
 Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 Db 1 MEKYNLGLVGEYSYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNGVADGVKSVLWOTLOALNFCIH 120
 Db 61 ENLVNLIEVCKKRWLVFEYCDHTLLNELRNPNGVADGVKSVLWOTLOALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGPAQIL-IPGDATYDVATRWYRAPPELLVGTQYG 179
 Db 121 NIHRDIKPENILVSQGVKLCDFGPAQIL-IPGDATYDVATRWYRAPPELLVGTQYG 179
 Qy 180 SSVDIWAGCVFAELLTQGPLWPKGSVDQYLYLIRTLGKLIIPRHQIFKSNFFHGISI 239
 Db 181 KAVDIWAGCVFAELLTQGPLWPKGSVDQYLYLIRTLGKLIIPRHQIFKSNFFHGISI 239
 Qy 240 PEPEDET--LEEFKFSVDVHPVAFNFMKGLKMPNDDRLTCSQLLESYF--DSF-----Q 290
 Db 241 PEVKDAEAEPLSEPKLPKPEAVISLAKKCLHIDPKRPFCDLRLHDFQMDGFAERFSQ 300
 Qy 291 EAQIK--RKARN-----EGRNRRQ 309
 Db 301 ELQKIEKDARNNSLPKKSQRKK 326

RESULT 13

Q9QUKO PRELIMINARY; PRT; 568 AA.
 AC Q9QUKO; 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Ser/Thr kinase KKIAMRE (Ser/Thr kinase KKIAMRE-beta).
 GN Name=Cdk12; Synonyms=Kkm;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; and C57BL/6; TISSUE=Brain;
 RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AB029073; BAA88439.1; JOINED.
 DR EMBL; AB029068; BAA88439.1; JOINED.
 DR EMBL; AB029069; BAA88439.1; JOINED.
 DR EMBL; AB029070; BAA88439.1; JOINED.
 DR EMBL; AB029072; BAA88439.1; JOINED.
 DR EMBL; AB029071; BAA88439.1; JOINED.
 DR EMBL; AB029065; BAA88427.1; JOINED.
 DR HSSP; P24941; IOIQ.
 DR MGD; MGI:1858227; Cdk12.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser thr pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 568 AA; 64055 MW; A43B75E2E9EB86C4 CRC64;

Query Match 56.0%; Score 930.5; DB 2; Length 568;
 Best Local Similarity 53.4%; Pred. No. 1.4e-57;
 Matches 174; Conservative 66; Mismatches 69; Indels 17; Gaps 6;
 Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 Db 1 MEKYNLGLVGEYSYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNGVADGVKSVLWOTLOALNFCIH 120
 Db 61 ENLVNLIEVCKKRWLVFEYCDHTLLNELRNPNGVADGVKSVLWOTLOALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGPAQIL-IPGDATYDVATRWYRAPPELLVGTQYG 179
 Db 121 NIHRDIKPENILVSQGVKLCDFGPAQIL-IPGDATYDVATRWYRAPPELLVGTQYG 179
 Qy 180 SSVDIWAGCVFAELLTQGPLWPKGSVDQYLYLIRTLGKLIIPRHQIFKSNFFHGISI 239
 Db 181 KAVDIWAGCVFAELLTQGPLWPKGSVDQYLYLIRTLGKLIIPRHQIFKSNFFHGISI 239
 Qy 240 PEPEDET--LEEFKFSVDVHPVAFNFMKGLKMPNDDRLTCSQLLESYF--DSF-----Q 290
 Db 241 PEVKDAEAEPLSEPKLPKPEAVISLAKKCLHIDPKRPFCDLRLHDFQMDGFAERFSQ 300
 Qy 291 EAQIK--RKARN-----EGRNRRQ 309
 Db 301 ELQKIEKDARNNSLPKKSQRKK 326

RESULT 14

Q9QY11 PRELIMINARY; PRT; 329 AA.
 AC Q9QY11;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ser/Thr kinase KIAA0842 (Fragment).
 GN Name=Cdk12; Synonyms=Kcm;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AB029067; BAA8429.1; -;
 DR HSP; P24941; 10IQ.
 DR MGD; MGI:185827; Cdk12.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW NON TER 329
 SQ SEQUENCE 329 AA; 38023 MW; F72EB8965AE8585 CRC64;

Query Match 55.8%; Score 928; DB 2; Length 329;
 Best Local Similarity 53.9%; Pred. No. 1.1e-57;
 Matches 173; Conservative 63; Mismatches 73; Indels 12; Gaps 5;

Qy 1 MEKYEKLAKTGEYSYGVVFKRNKTSQVAVKFFVESEDDPVVKIALREIRMLKQLKH 60
 Db 1 MEKYNLGLVGEYSYGVVFKRNKTSQVAVKFFVESEDDPVVKIALREIRMLKQLRH 60
 Qy 61 PNLVNLLEVPFRKRMHLVFEYCDHTLLNELRNPNVGVKSVLQALNFCFHH 120
 Db 61 ENLVNLLEVCCKRWYLVFEVDHTLLDLKLPNGLDYQVVKYLFQINGIGFCHSH 120
 Qy 121 NCHRDIKPENILTKGIIKICDFGPAQL-IPGDAYTDVATRWVRAPELLVGDYQYG 179
 Db 121 NIHRDIPENILVSGVQVWKLCDGFGFARTLAPEVITDVTATRWVRAPELLVGDYQYG 180
 Qy 180 SSVDIWAIGCVFARLLTQCPILWPKSGSDVDQYLIIRTLGLKLIPIHQSIKSNFFHGISI 239
 Db 181 KAVDIWAIGCLVIEMLGQPLPFGESDIDQLHMTCLGNLIPRQELFYKNPVPAGVRL 240
 Qy 240 PEPEDMET--LEEKFSVDHVPALNFMKGLKMPNDDRLTCSQLLESSYF--DSF-----Q 290
 Db 241 PEVKDAEAEPLSEYKPLPEAVISLAKKCLHIDDKPFCADLLRHDFQMDGFAERFSQ 300
 Qy 291 EAQIK--RKARNEGRRRQ 309
 Db 301 ELQKIEKDANNSLPKKSQK 321

RESULT 15

Q6GMD6 PRELIMINARY; PRT; 320 AA.
 AC Q6GMD6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE LOC443693 protein (Fragment).
 GN Name=LOC443693;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 Klein S., Gerhard D.S.;
 Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 320
 SQ SEQUENCE 320 AA; 37063 MW; 4CD2189603F9115F CRC64;

Query Match 55.8%; Score 924; DB 2; Length 320;

```

Best Local Similarity 53.8%; Pred. No. 2.1e-57;
Matches 169; Conservative 64; Mismatches 75; Indels 6; Gaps 3;
QY 1 MEKYEKLAGTGGSYGVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYNLGLVGGSYGMVMKCRNKETGRIVAKTFLESEDDKRVKKIAMREIKLLKQLRH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELEERNPNGVADGVIKSVLMQTLQALNFCIH 120
Db 61 ENLVNLLEVCKKKRWYLVFEVDRTVLDLEQFNGLDFNRVKYLFQIRGIGFCHNH 120
QY 121 NCIHRDIKENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NCIHRDIKENILVSLGIVKLCDFGARTLAGPGEDYTDYVATRWYRAPELLVGDIKYG 180
QY 180 SSVDIWAIGCVFAELLTGOPLWPKSDVDOLYLIIRTGLKLIPIHQSIKNGPFGISI 239
Db 181 KAVDWAIGCVITVEMLTQAQPLFPFGSDIDQLHHIIKCGNLTPRHQELFYRNPMFAGVSL 240
QY 240 PEPEDMETLEKFSVDVHPVALNFMKGCLKMNPPDDRLTCSQLLESSYF--DSFQE---AQI 294
Db 241 PMKEAESLERYPKHSPWMLDLAKSLHIDPEKEPCACGTLLQHELFTKDNFSEFSGEI 300
QY 295 KKARNEGNRRRQ 308
Db 301 RAKLQNLKDNSSQ 314

```

Search completed: April 22, 2005, 06:50:40
Job time : 83.7946 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:23:15 ; Search time 96.4471 Seconds
(without alignments)
1391.497 Million cell updates/sec

Title: US-10-766-691-10
Perfect score: 1820
Sequence: 1 MEKYEKLAKTGEYSYGVFK.....RKARNEGRNRRRQQLPLKS 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1820	100.0	347	4	AAE00494 Human kin
2	1796	98.7	356	4	AAE00491
3	1636	89.9	315	4	AAE00495 Human kin
4	1613	88.6	342	5	AAE19152 Human kin
5	1612	88.6	324	4	AAE00492 Human kin
6	1593	87.5	360	4	AAU03525 Human pro
7	1270.5	69.8	296	4	AAE00494 Novel pro
8	1270.5	69.8	296	4	AAE00494 Novel pro
9	1162.5	63.9	358	5	ABP62954 Human pol
10	1157.5	63.6	358	8	ADO01538 Human cyc
11	1134	62.3	228	5	AAE00494 Human kin
12	1123	61.7	247	4	AAE00494 Novel pro
13	1123	61.7	247	8	ADI29249 Human MAR
14	1001.5	55.0	392	4	ABB63118 Drosophil
15	948	52.1	197	6	ABU11689 Human MDD
16	941.5	51.7	566	3	AAE00494 Rabbit KK
17	915.5	50.3	493	7	ADU77659 Human 162
18	915.5	50.3	493	8	ADU77659 Human 162
19	911.5	50.1	362	6	ABP6087 Human pro
20	825.5	45.6	183	8	ADI40875 Human kin
21	791	43.5	187	4	AAE00494 Human kin
22	791	43.5	198	4	AAE00493 Human kin
23	791	43.5	205	8	ADU71868 Human kin
24	758.5	41.7	455	3	AAE00494 Human los
25	758.5	41.7	455	8	ADI57233 NKIAMRE d

26	758.5	41.7	455	8	ADI57214
27	758.5	41.7	455	8	ADI57236
28	758.5	41.7	591	4	AAU03524
29	737.5	40.5	457	3	AAE00494 Rat lost
30	737.5	40.5	505	3	AAE00494 Rat lost
31	712.5	39.1	154	6	ABU05290 Human dia
32	699	38.4	562	8	ABM83922 Human dia
33	666	36.6	534	4	AAE00494 Novel pro
34	666	36.6	534	8	ADI29252 Human MAR
35	569	31.3	224	4	ABG06142 Novel hum
36	565	31.0	305	7	ADJ45039 Human kin
37	565	31.0	305	7	ADJ68738 Human hea
38	565	31.0	305	8	ADI57200 Human CDK
39	565	31.0	305	8	ADI57237
40	565	31.0	333	4	AAE00494 Human pol
41	563	30.9	544	2	AAE00494 CDK2-gree
42	558	30.7	352	4	AAE00494 Human pol
43	557	30.6	298	2	AAE00494 Homo sapi
44	557	30.6	544	2	AAE00494 Green flu
45	556	30.5	298	7	ADD21390 Human cyc

ALIGNMENTS

RESULT 1
AAE00494
ID AAE00494 standard; protein; 347 AA.
AC AAE00494;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human kinase #5.
XX
KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
XX
OS Homo sapiens.
XX
PN WO200123579-A1.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026621.
XX
PR 28-SEP-1999; 99US-0156511P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI; 2001-266166/27.
DR N-PSDB; AAD03816.
XX
PT New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
PS Claim 2; Page 32-33; 38pp; English.
XX
CC The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical

CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
 CC probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 347 AA;

Query Match 100.0%; Score 1820; DB 4; Length 347;
 Best Local Similarity 100.0%; Pred. No. 1.6e-186;
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
 DB |||||
 QY 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
 DB |||||
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 DB |||||
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 DB |||||
 QY 121 NCIHRIKPENILITKQGIKICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
 DB |||||
 QY 121 NCIHRIKPENILITKQGIKICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
 DB |||||
 QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB |||||
 QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB |||||
 QY 241 VASQAGITGKLI PRHQSIKSNFGFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
 DB |||||
 QY 241 VASQAGITGKLI PRHQSIKSNFGFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
 DB |||||
 QY 301 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 347
 DB |||||
 QY 301 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 347
 DB |||||

RESULT 2
 AAE00491
 ID AAE00491 standard; protein; 356 AA.
 AC AAE00491;
 XX
 XX
 XX
 XX 19-JUN-2001 (first entry)
 XX Human kinase #2.
 DE Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder.
 XX Homo sapiens.
 OS
 XX WO200123579-A1.
 XX
 XX 05-APR-2001.
 XX
 XX 27-SEP-2000; 2000WO-US026621.
 XX
 XX 28-SEP-1999; 99US-0156511P.
 XX
 XX (LEXI-) LEXICON GENETICS INC.
 XX
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 FI
 XX WPI; 2001-266166/27.
 DR N-PSDB; AAD03813.
 XX
 XX New isolated human kinase polynucleotide useful for generating

PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX
 PS Disclosure; Page 28-29; 38pp; English.
 XX
 CC The present sequence is novel human protein (NHP) known as human kinase.
 CC The human kinases share structural similarity with animal kinases, more
 CC particularly serine or threonine protein kinases. Human kinase cDNA is
 CC useful for the detection of mutant human kinase for the diagnosis of
 CC disease, and also as a therapeutic. It is useful for screening drugs
 CC effective in the treatment of symptomatic or phenotypic manifestations
 CC perturbing the normal function of NHP in the body. The NHP nucleotide
 CC sequences are useful for generation of antibodies, as reagents in
 CC diagnostic assays, for the identification of other cellular gene products
 CC related to human kinases, and as reagents in assays for screening
 CC compounds that are useful for treating mental, biological or medical
 CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
 CC probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 356 AA;

Query Match 98.7%; Score 1796; DB 4; Length 356;
 Best Local Similarity 100.0%; Pred. No. 6.5e-184;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
 DB |||||
 QY 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
 DB |||||
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 DB |||||
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 DB |||||
 QY 121 NCIHRIKPENILITKQGIKICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
 DB |||||
 QY 121 NCIHRIKPENILITKQGIKICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
 DB |||||
 QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB |||||
 QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB |||||
 QY 241 VASQAGITGKLI PRHQSIKSNFGFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
 DB |||||
 QY 241 VASQAGITGKLI PRHQSIKSNFGFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
 DB |||||
 QY 301 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 342
 DB |||||
 QY 301 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 342
 DB |||||

RESULT 3
 AAE00495
 ID AAE00495 standard; protein; 315 AA.
 AC AAE00495;
 XX
 XX
 XX 19-JUN-2001 (first entry)
 XX Human kinase #6.
 DE Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder.
 XX Homo sapiens.
 OS
 XX WO200123579-A1.

XX PD 05-APR-2001.
 XX PF 27-SEP-2000; 2000WO-US026621.
 XX PR 28-SEP-1999; 99US-0156511P.
 XX PA (LEXI-) LEXICON GENETICS INC.
 XX PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 XX PI Sands AT;
 XX XX
 XX DR WPI: 2001-266166/27.
 XX DR N-PSDB: AAD03817.
 XX PT New isolated human kinase polynucleotide useful for generating
 XX PT antibodies, as reagents in diagnostic assays and for screening for
 XX PT compounds useful for treating mental, biological or medical diseases.
 XX PS
 XX PS Claim 3; Page 33-34; 38pp; English.
 XX CC The present sequence is novel human protein (NHP) known as human kinase.
 XX CC The human kinases share structural similarity with animal kinases, more
 XX CC particularly serine or threonine protein kinases. Human kinase cDNA is
 XX CC useful for the detection of mutant human kinase for the diagnosis of
 XX CC disease, and also as a therapeutic. It is useful for screening drugs
 XX CC effective in the treatment of symptomatic or phenotypic manifestations
 XX CC perturbing the normal function of NHP in the body. The NHP nucleotide
 XX CC sequences are useful for generation of antibodies, as reagents in
 XX CC diagnostic assays, for the identification of other cellular gene products
 XX CC related to human kinases, and as reagents in assays for screening
 XX CC compounds that are useful for treating mental, biological or medical
 XX CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
 XX CC probes are useful for screening human genomic library for identifying
 XX CC polymorphisms and as primers in amplification assays to detect mutations
 XX CC within the exons, introns and splice sites that can be used in
 XX CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 XX CC products are used to genetically engineer cells in vivo that functions as
 XX CC bioreactors in the body delivering a continuous supply of NHP to the
 XX CC body. Nucleotide constructs encoding functional NHPs are used in gene
 XX CC therapy for the modulation of NHP expression
 XX S0 Sequence 315 AA;
 Query Match 89.9%; Score 1636; DB 4; Length 315;
 Best Local Similarity 90.8%; Pred. No. 9e-167;
 Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKTALREIRMLKOLKH 60
 Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKTALREIRMLKOLKH 60
 Qy 61 PNLVNLLEVFRRKRMHLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH 120
 Db 61 PNLVNLLEVFRRKRMHLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH 120
 Qy 121 NCIHRIKPENILITKQGIKICDFGAQILIPGDAYTDYVATRYRAPELLVGDTOYGS 180
 Db 121 NCIHRIKPENILITKQGIKICDFGAQILIPGDAYTDYVATRYRAPELLVGDTOYGS 180
 Qy 181 SVDIWAIGCVFAELLTGOPLWPGKSDVDQLYIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Db 181 SVDIWAIGCVFAELLTGOPLWPGKSDVDQLYIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Qy 241 VASQAGITGKLIIRHOSIFKSNCFEFGISIPEDMETLLEKSDVHPVALNFMKGLK 300
 Db 241 VASQAGITGKLIIRHOSIFKSNCFEFGISIPEDMETLLEKSDVHPVALNFMKGLK 300
 Qy 301 MNPDRLTCSQLLESSYFDSFQEAQIKKARNEGRRNRQOVLPLKS 347
 Db 269 MNPDRLTCSQLLESSYFDSFQEAQIKKARNEGRRNRQOVLPLKS 315

RESULT 4
 AAE19152
 ID AAE19152 standard; protein; 342 AA.
 XX AC AAE19152;
 XX DT 21-MAY-2002 (first entry)
 XX DE Human kinase polypeptide (PKIN-10).
 XX KW Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease;
 KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
 KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
 KW cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
 KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
 KW hypotensive; anti-HIV; enzyme.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 4..286
 FT /note= "Eukaryotic protein kinase domain"
 XX WO200208399-A2.
 XX 31-JAN-2002.
 XX 20-JUL-2001; 2001WO-US023092.
 XX 21-JUL-2000; 2000US-0220038P.
 XX 28-JUL-2000; 2000US-0222112P.
 XX 04-AUG-2000; 2000US-0222831P.
 XX 11-AUG-2000; 2000US-0224729P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX (THOR-) THORNTON M.
 XX Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;
 XX Patterson C, Rankumar J, Gandhi AR, Policky JL, Baughn MR;
 XX Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
 XX Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
 XX Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
 XX WPI: 2002-206083/26.
 XX N-PSDB: AAD30557.
 XX New human kinase polypeptide, useful in diagnosis, prevention and
 XX treatment of cancer, immune disorder, growth and developmental disorder,
 XX cardiovascular disorder and lipid disorder.
 XX Claim 1; Page 147-148; 196pp; English.
 XX The present invention relates to an isolated human kinase polypeptide
 XX (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
 XX useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
 XX lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
 XX syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 XX disease, rheumatoid arthritis), a growth and developmental disorder (e.g.,
 XX bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
 XX cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 XX infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
 XX Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 XX drug screening techniques and to analyse the proteome of a tissue or cell
 XX type. PKIN is useful for creating knockin humanised animals or transgenic
 XX animals to model human diseases, in somatic or germline gene therapy, to
 XX generate a transcript image of a tissue or cell type, for detecting
 XX differences in the chromosomal location due to translocation, inversion,
 XX etc., among normal, carrier or affected individuals, and as hybridisation
 XX probes for mapping naturally occurring genomic sequences. PKIN is useful
 XX in southern or northern analysis, dot blot or other membrane-based

CC technologies, in PCR technologies, in dipstick, pin, multiformat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-10
 XX
 SQ Sequence 342 AA;
 Query Match 88.6%; Score 1613; DB 5; Length 342;
 Best Local Similarity 89.9%; Pred. No. 3.1e-164;
 Matches 312; Conservative 1; Mismatches 0; Indels 34; Gaps 2;
 QY 1 MEKYEKLAKTGGSGYGVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
 DB 1 MEKYEKLAKTGGSGYGVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDVATRWYRAPELLVGDTOYGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 QY 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGLK 300
 DB 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGLK 300
 QY 301 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV--QVLPL 345
 DB 269 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV--QVLPL 315
 RESULT 5
 ID AAE00492
 AC AAE00492;
 DT 19-JUN-2001 (first entry)
 DE Human kinase #3.
 KW Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder.
 XX Homo sapiens.
 OS WO200123579-A1.
 PN 05-APR-2001.
 PD 27-SEP-2000; 2000WO-US026621.
 PE 28-SEP-1999; 99US-0156511P.
 PR (LEXI-) LEXICON GENETICS INC.
 PA Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 PI WPI; 2001-266166/27.
 DR N-PSDB; AAD03814.
 XX New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX Disclosure; Page 30; 38pp; English.

CC The present sequence is novel human protein (NHP) known as human kinase.
 CC The human kinases share structural similarity with animal kinases, more
 CC particularly serine or threonine protein kinases. Human kinase cDNA is
 CC useful for the detection of mutant human kinase for the diagnosis of
 CC disease, and also as a therapeutic. It is useful for screening drugs
 CC effective in the treatment of symptomatic or phenotypic manifestations
 CC perturbing the normal function of NHP in the body. The NHP nucleotide
 CC sequences are useful for generation of antibodies, as reagents in
 CC diagnostic assays, for the identification of other cellular gene products
 CC related to human kinases, and as reagents in assays for screening
 CC compounds that are useful for treating mental, biological or medical
 CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
 CC probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 324 AA;
 Query Match 88.6%; Score 1612; DB 4; Length 324;
 Best Local Similarity 90.6%; Pred. No. 3.6e-164;
 Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 QY 1 MEKYEKLAKTGGSGYGVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
 DB 1 MEKYEKLAKTGGSGYGVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDVATRWYRAPELLVGDTOYGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 QY 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGLK 300
 DB 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGLK 300
 QY 301 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV 342
 DB 269 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV 310
 RESULT 6
 ID AAU03525
 AC AAU03525;
 DT 12-SEP-2001 (first entry)
 DE Human protein kinase #25.
 DE Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder.
 XX Homo sapiens.
 OS WO200138503-A2.
 PN 31-MAY-2001.
 PD 31-MAY-2001.

PF 22-NOV-2000; 2000WO-US032085.
XX
PR 24-NOV-1999; 99US-0167482P.
XX
XX
PA (SUGE-) SUGEN INC.
XX
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
XX WPI; 2001-343950/36.
DR N-PSDB; AAS06725.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
FT neuronal-associated diseases, and microbial infections.
XX
XX
PS Claim 7; Fig 2; 433pp; English.
XX
XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 360 AA;

Query Match 87.5%; Score 1593; DB 4; Length 360;
Best Local Similarity 85.2%; Pred. No. 4.7e-162;
Matches 311; Conservative 2; Mismatches 0; Indels 52; Gaps 3;

Qy 1 MEKYEKLAKTGECSGVVFKCRNKTSGQVAVKVFVESEDDPVVKKTALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGECSGVVFKCRNKTSGQVAVKVFVESEDDPVVKKTALREIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVLFVEYCDHTLLNELRPNPGVADGVKSVLWOTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMHVLFVEYCDHTLLNELRPNPGVADGVKSVLWOTLQALNFCCHI 120

Qy 121 NCIHRIKPNILITKQGIKICDFGFAQIL-----IPGDAYTDYVA 162
Db 121 NCIHRIKPNILITKQGIKICDFGFAQILNSHVGRIDLPLDIDAPAVPGDAYTDYVA 180

Qy 163 TRWYRAPPELLVGDYQYSSVDIWAIGCVFABLLTGQPLWPKSDVDQYLIIRLTVEGTF 222
Db 181 TRWYRAPPELLVGDYQYSSVDIWAIGCVFABLLTGQPLWPKSDVDQYLIIRLT----- 235

Qy 223 RHVDQAGLELLTSDPPPAVASQSAGITCKLIPRQSIKSNFGFHGISIPEPEDETLEE 282
Db 236 -----GKLIIPRQSIKSNFGFHGISIPEPEDETLEE 268

Qy 283 KFSVDVHPVALFMKGLKQNPDDRLTCSQLLESSYFDSFQBAQIKRKARNEGRRRQ-- 340
Db 269 KFSVDVHPVALFMKGLKQNPDDRLTCSQLLESSYFDSFQBAQIKRKARNEGRRRQON 328

Qy 341 QVLPL 345
Db 329 QLLPL 333

RESULT 7
AAB65643

ID AAB65643 standard; protein; 296 AA.
XX
AC AAB65643;
XX
XX 27-MAR-2001 (first entry)
XX
XX Novel protein kinase, SEQ ID NO: 170.
XX
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiaethmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Mus musculus.
XX
XX WO200073469-A2.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US014842.
XX
XX 28-MAY-1999; 99US-0136503P.
XX
XX (SUGE-) SUGEN INC.
XX
XX Plowman GD, Martinez R, Whyte D, Sudarsanam S;
XX
XX WPI; 2001-032161/04.
XX N-PSDB; AAF44670.
XX
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
FT neurodegenerative diseases and/or cancers.
XX
XX Claim 10; Fig 1; 310pp; English.
XX
XX The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 296 AA;

Query Match 69.8%; Score 1270.5; DB 4; Length 296;
Best Local Similarity 80.5%; Pred. No. 1.8e-127;
Matches 243; Conservative 19; Mismatches 5; Indels 35; Gaps 3;

Qy 46 KIALREIRMLKQLKHPNLVNLIEVFRKRKMHVLFVEYCDHTLLNELRPNPGVADGVKS 105
Db 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKMHVLFVEYCDHTLLNELRPNPGVADGVKS 59

Qy 106 VLWOTLQALNFCCHIHCIRHDIKPENILITKQGIKICDFGFAQILPGDAYTDYVATRW 165
Db 60 VLWOTLQALNFCCHKNCIHRDVKPENILITKQGIKICDFGFAQILPGDAYTDYVATRW 119

Qy 166 YRAPPELLVGDYQYSSVDIWAIGCVFABLLTGQPLWPKSDVDQYLIIRLTVEGTFRH 225
Db 120 YRAPPELLVGDYQYSSVDVWAVGCVFABLLTGQPLWPKSDVDQYLIIRLT----- 171

QY 226 DQAGLELTSSDPPAVASQSAGITGKLI PRHQSIKSNQFFHGHSIPEPEMETLEEKFS 285
 Db 172 -----GKLI PRHQSIKSNQFFHGHSIPEPEMETLEEKFS 207

QY 286 DVHPVALNFMKGLKMNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRNRRO--QVL 343
 Db 208 NVQPVALSFMKGLKMNPDRLTCAQLDSAYFESFOEDQMKRKARSEGRSRRRQONQLL 267

QY 344 PL 345
 Db 268 PL 269

RESULT 8
 ADI29250
 ID ADI29250 standard; protein; 296 AA.
 AC ADI29250;
 XX 22-APR-2004 (first entry)
 DT Mouse MARK3-associated protein #12.
 DE
 XX Mouse; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX
 OS Mus musculus.
 XX
 FN US2003232771-A1.
 PD 18-DEC-2003.
 XX
 PF 17-JUN-2002; 2002US-00174319.
 XX
 PR 17-JUN-2002; 2002US-00174319.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 PI Ward DT, Freier SM, Dobie KW;
 XX WPI; 2004-052188/05.
 DR N-PSDB; ADI29368.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 170; 233pp; English.
 XX
 CC The invention relates to a compound comprising a sequence comprising 8-80
 CC base pairs (bp) targeted to a nucleic acid encoding MARK3
 CC (MAP/microtubule affinity-regulating kinase 3), that specifically
 CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
 CC composition comprising the compound and a carrier or diluent, inhibiting
 CC the expression of MARK3 in cells or tissues, treating an animal having or
 CC suspected of having a disease or condition associated with MARK3 and
 CC screening for an antisense compound. The antisense oligonucleotide is
 CC useful for preparing a composition for treating hyperproliferative
 CC disorder, particularly cancer and neurodegenerative diseases e.g.
 CC Alzheimer's disease. The present sequence is a MARK3 associated protein
 CC included in the figures but not mentioned anywhere else in the
 CC specification.
 XX
 SQ Sequence 296 AA;
 Query March 69.8%; Score 1270.5; DB 8; Length 296;
 Best Local Similarity 80.5%; Pred. No. 1.8e-127;
 Matches 243; Conservative 19; Mismatches 5; Indels 35; Gaps 3;

QY 46 KIALREIRMLKQLKHPNLVNLIEVFRKRKRKHLVFEYCDHTLLNELERNPNVADGVIKS 105
 Db 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKRKHLVFEYCDHTLLNELERNPNVADGVIKS 59

QY 106 VLWQTLQALNFCNCHNCIHRDIKBNILITKQGIKICDQFGAQILIPGDAYTYVATRW 165
 Db 60 VLWQTLQALNFCNCHNCIHRDVKPENILITKQGMIKICDQGFARILIPGDAYTYVATRW 119

QY 166 YRAPPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIIRTLVETGRHV 225
 Db 120 YRAPPELLVGDYQYSSVDVWAVGCVFAELLTGQPLWPKGSDVDQYLIIIRTL 171

QY 226 DQAGLELTSSDPPAVASQSAGITGKLI PRHQSIKSNQFFHGHSIPEPEMETLEEKFS 285
 Db 172 -----GKLI PRHQSIKSNQFFHGHSIPEPEMETLEEKFS 207

QY 286 DVHPVALNFMKGLKMNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRNRRO--QVL 343
 Db 208 NVQPVALSFMKGLKMNPDRLTCAQLDSAYFESFOEDQMKRKARSEGRSRRRQONQLL 267

QY 344 PL 345
 Db 268 PL 269

RESULT 9
 ABP62954
 ID ABP62954 standard; protein; 358 AA.
 AC ABP62954;
 XX 14-OCT-2002 (first entry)
 DT Human polypeptide SEQ ID NO 391.
 XX
 DE Human; vulnery; dermatological; neuroprotective; immunosuppressive; cancer;
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 XX
 OS Homo sapiens.
 XX
 FN WO200218424-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-US027093.
 XX
 PR 01-SEP-2000; 2000US-00654935.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
 XX WPI; 2002-583321/62.
 DR N-PSDB; ABQ93433.
 XX
 PT New polynucleotide and polypeptides, useful for treatment and diagnosis
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies.
 XX
 PS Claim 20; SEQ ID NO 391; 284pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising one of
 CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 CC (I) is useful for gene therapy of diseases and (II) can be used for

CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 358 AA;

Query Match 63.9%; Score 1162.5; DB 5; Length 358;
 Best Local Similarity 63.8%; Pred. No. 1e-115;
 Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;
 Qy 1 MEKYEKAKTGEISGVVFKCRNKTSGQVAVKFESEDDPVVKIALREIRMLKQLKH 60
 Db 2 MEKYEKIGKIGESGVVFKCRNRTGQIVAKKFESEDDPVVKIALREIRMLKQLKH 61
 Qy 61 PNLVNLLEVFRRKRRLHLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCHH 120
 Db 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHBLDRYQGVPEHLVKSITWQTLQAVNFCCHK 121
 Qy 121 NCIRHDIKPENILITKQGIKICDFGPAQILI - PGDAYTDVATRWYRAPPELLVGDQY 179
 Db 122 NCIRHDVAPENILITKHSVILKCLDFGFAFLTGTGSDYTDVATRWSPPELLVGDQY 181
 Qy 180 SSVDIWAGCVFAELLTGQPLWPGKSDVDQLYLIRTLVETGFRHVDAQLELLTSSDPP 239
 Db 182 PPVDVWAGCVFAELLTGQPLWPGKSDVDQLYLIRKTL - - - - - 219
 Qy 240 AVASQASGITKGLIPRHQSIFKNGFPHGISIPPEMETLEKFSVHPVAFNMKGCL 299
 Db 220 - - - - - GDLIPRHQQVSTNQYFSGVKIPDPEDMEPLEKFPNISYPALGLKGL 269
 Qy 300 KMPDRLTCSOLLESSYFDSFQEAQ 333
 Db 270 HMDPTERTLTCQLLHPYFENIREIEDLAKBNK 303

RESULT 10
 AD001538
 ID AD001538 standard; protein; 358 AA.
 XX
 AC AD001538;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human cyclin-dependent kinase like 1 (CDKL1) protein SEQ ID NO:4.
 XX human; cyclin-dependent kinase like 1; CDKL1; branching morphogenesis;
 XX branching morphogenesis modulator; angiogenic disorder;
 KW apoptotic disorder; proliferation disorder; chromosome 14.
 XX
 OS Homo sapiens.
 XX
 FN WO2004038372-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 22-OCT-2003; 2003WO-US033483.
 XX
 PR 23-OCT-2002; 2002US-0420554P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Plowman GD, Karim PD, Swimmer C, Habeck HA, Koblizek TI;
 PI Schulte-Merker S, Langheinrich U, Stott CM, Trowe T, Vogel AM;
 PI Odenthal JH, Scheel JK, Will TT, Jin Y, Hai B;
 XX
 DR WPI; 2004-365563/34.
 DR N-PSDB; ADO01535.
 XX

PT Use of cyclin-dependent kinase like 1 polypeptides or nucleic acids for
 PT modulating branching morphogenesis in a mammalian cell or for diagnosing
 PT a disease e.g. angiogenic, apoptotic or proliferation disorder in a
 PT patient.
 XX
 PS Example; SEQ ID NO 4; 52pp; English.

XX
 CC The present invention describes the use of a cyclin-dependent kinase like
 CC 1 (CDKL1) polypeptide or nucleic acid for modulating branching
 CC morphogenesis in a mammalian cell or for diagnosing a disease in a
 CC patient. Also described: (1) identifying a candidate branching
 CC morphogenesis modulating agent; (2) modulating branching morphogenesis in
 CC a mammalian cell comprising contacting the cell with an agent that
 CC specifically binds a CDKL1 polypeptide or nucleic acid; and (3) a method
 CC for diagnosing a disease in a patient. The CDKL1 polypeptide or nucleic
 CC acid is useful for modulating branching morphogenesis in a mammalian
 CC cell. It is also useful for diagnosing a disease, e.g. angiogenic,
 CC apoptotic or proliferation disorder in a patient. The present sequence
 CC represents human CDKL1, which is used in the exemplification of the
 CC present invention. The human CDKL1 gene is located on chromosome 14, more
 CC specifically to 14q22.1.

XX Sequence 358 AA;

Query Match 63.8%; Score 1157.5; DB 8; Length 358;
 Best Local Similarity 64.7%; Pred. No. 3.6e-115;
 Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;
 Qy 1 MEKYEKAKTGEISGVVFKCRNKTSGQVAVKFESEDDPVVKIALREIRMLKQLKH 60
 Db 2 MEKYEKIGKIGESGVVFKCRNRTGQIVAKKFESEDDPVVKIALREIRMLKQLKH 61
 Qy 61 PNLVNLLEVFRRKRRLHLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCHH 120
 Db 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHBLDRYQGVPEHLVKSITWQTLQAVNFCCHK 121
 Qy 121 NCIRHDIKPENILITKQGIKICDFGPAQILI - PGDAYTDVATRWYRAPPELLVGDQY 179
 Db 122 NCIRHDVAPENILITKHSVILKCLDFGFAFLTGTGSDYTDVATRWSPPELLVGDQY 181
 Qy 180 SSVDIWAGCVFAELLTGQPLWPGKSDVDQLYLIRTLVETGFRHVDAQLELLTSSDPP 239
 Db 182 PPVDVWAGCVFAELLTGQPLWPGKSDVDQLYLIRKTL - - - - - 219
 Qy 240 AVASQASGITKGLIPRHQSIFKNGFPHGISIPPEMETLEKFSVHPVAFNMKGCL 299
 Db 220 - - - - - GDLIPRHQQVSTNQYFSGVKIPDPEDMEPLEKFPNISYPALGLKGL 269
 Qy 300 KMPDRLTCSOLLESSYFDSFQEAQ 325
 Db 270 HMDPTERTLTCQLLHPYFENIREIE 295

RESULT 11
 AAG78547
 ID AAG78547 standard; protein; 228 AA.
 XX
 AC AAG78547;
 XX
 DT 08-MAR-2002 (first entry)
 XX
 DE Human kinase 14257 amino acid sequence.
 XX
 KW Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;
 KW antidiabetic; neuroprotective; antiarthritic; dermatological;
 KW immunosuppressive; antiinflammatory; antithyroid; antipsoriatic;
 KW ophthalmological; antiallergic; antiasthmatic; antiatherosclerotic;
 KW hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic;
 KW immunomodulator; analgesic; cellular proliferative disorder; cancer;
 KW acute lymphoblastic leukaemia; Hodgkin's disease;
 KW bone metabolism disorder; osteoporosis; immune system disorder;
 KW inflammatory; diabetes mellitus; osteoarthritis; asthma;
 KW cardiovascular disorder; hypertension; coronary artery disease;

Search completed: April 22, 2005, 06:47:31
Job time : 101.447 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 04:37:19 ; Search time 34.071 Seconds
(without alignments)
760.272 Million cell updates/sec

Title: US-10-766-691-10

Perfect score: 1820

Sequence: 1 MEKYEKLAKTGEYSYGVVFK.....RKARNEGRRRQOVLPKLS 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:**
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:**
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:**
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:**
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1820	100.0	347	4	US-09-671-050-10
2	1796	98.7	356	4	US-09-671-050-4
3	1636	89.9	315	4	US-09-671-050-12
4	1612	88.6	324	4	US-09-671-050-6
5	1162.5	63.9	367	4	US-09-949-016-7552
6	1157.5	63.6	358	4	US-09-411-628-11
7	1157.5	63.6	358	4	US-10-174-794-11
8	941.5	51.7	566	4	US-09-411-628-4
9	941.5	51.7	566	4	US-10-174-794-4
10	915.5	50.3	475	4	US-09-949-016-7954
11	915.5	50.3	493	4	US-09-411-628-10
12	915.5	50.3	493	4	US-10-174-794-10
13	791	43.5	187	4	US-09-671-050-2
14	791	43.5	198	4	US-09-671-050-8
15	565	31.0	305	4	US-09-538-092-1236
16	565	31.0	305	4	US-09-949-016-6052
17	565	31.0	334	4	US-09-949-016-10777
18	563	30.9	544	4	US-09-417-197-113
19	557	30.6	298	2	US-08-874-347-25
20	557	30.6	298	2	US-08-969-106-2
21	557	30.6	298	3	US-09-093-522-25
22	557	30.6	298	4	US-09-338-125-2
23	557	30.6	298	4	US-09-266-225D-14
24	557	30.6	544	4	US-09-417-197-115
25	556	30.5	298	4	US-09-411-628-13
26	556	30.5	298	4	US-10-174-794-13
27	554	30.4	297	1	US-08-176-620A-16

28	554	30.4	297	2	US-08-461-985-16	Sequence 15, Appl
29	554	30.4	298	3	US-09-457-040B-29	Sequence 29, Appl
30	554	30.4	298	4	US-09-538-092-1006	Sequence 1006, Ap
31	554	30.4	354	4	US-09-949-016-8025	Sequence 8025, Ap
32	551.5	30.3	294	2	US-08-874-347-26	Sequence 26, Appl
33	551.5	30.3	294	3	US-09-093-522-26	Sequence 26, Appl
34	547.5	30.1	270	2	US-07-857-224B-31	Sequence 31, Appl
35	545	29.9	297	2	US-08-874-347-24	Sequence 24, Appl
36	545	29.9	297	3	US-09-093-522-24	Sequence 24, Appl
37	545	29.9	297	4	US-09-411-628-12	Sequence 12, Appl
38	545	29.9	297	4	US-10-174-794-12	Sequence 12, Appl
39	541	29.7	297	2	US-08-874-347-23	Sequence 23, Appl
40	541	29.7	297	3	US-09-093-522-23	Sequence 23, Appl
41	540	29.7	274	1	US-08-318-947A-20	Sequence 20, Appl
42	540	29.7	274	2	US-08-795-303-20	Sequence 20, Appl
43	540	29.7	299	4	US-09-949-016-10673	Sequence 10673, A
44	538.5	29.6	300	2	US-08-874-347-10	Sequence 10, Appl
45	538.5	29.6	300	3	US-09-093-522-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-671-050-10
; Sequence 10, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 347
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-10

Query Match	100.0%;	Score 1820;	DB 4;	Length 347;
Best Local Similarity	100.0%;	Pred. No. 2.4e-186;		
Matches 347;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEKYEKLAKTGEYSYGVVFKCRNKTSQGVAVKVFVESEDDPVVKTKALREIRMLKQLKH	60	
Db	1	MEKYEKLAKTGEYSYGVVFKCRNKTSQGVAVKVFVESEDDPVVKTKALREIRMLKQLKH	60	
Qy	61	PNLVNLIEVFRKRKMHLPVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH	120	
Db	61	PNLVNLIEVFRKRKMHLPVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH	120	
Qy	121	NCIHRDIKPENILTKQGIKICDFGPAQLIPGDAYTDVYVATRYRAPELLVGDQYGS	180	
Db	121	NCIHRDIKPENILTKQGIKICDFGPAQLIPGDAYTDVYVATRYRAPELLVGDQYGS	180	
Qy	181	SVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLVETGFRVHQAGLELLSSDPPA	240	
Db	181	SVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLVETGFRVHQAGLELLSSDPPA	240	
Qy	241	VASQAGITGKLIIPRHOSIFKSNGFHGISIPEPEDMETLEEKFSVDHPVALNFMKGLK	300	
Db	241	VASQAGITGKLIIPRHOSIFKSNGFHGISIPEPEDMETLEEKFSVDHPVALNFMKGLK	300	

QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRQQVPLPKS 347
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRQQVPLPKS 347

RESULT 2

US-09-671-050-4
; Sequence 4, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-4

Query Match 98.7%; Score 1796; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 9.2e-184;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELRPNPGVADGVKSVLWOTLQALNFCIH 120
Db 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELRPNPGVADGVKSVLWOTLQALNFCIH 120
QY 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 241 VASQSAGITGKLIIPRHOSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
Db 241 VASQSAGITGKLIIPRHOSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRQQV 342
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRQQV 342

RESULT 3

US-09-671-050-12
; Sequence 12, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 315
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-12

Query Match 89.9%; Score 1636; DB 4; Length 315;
Best Local Similarity 90.8%; Pred. No. 1.1e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELRPNPGVADGVKSVLWOTLQALNFCIH 120
Db 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELRPNPGVADGVKSVLWOTLQALNFCIH 120
QY 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 241 VASQSAGITGKLIIPRHOSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
Db 241 VASQSAGITGKLIIPRHOSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRQQVPLPKS 315
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRQQVPLPKS 315

RESULT 4

US-09-671-050-6
; Sequence 6, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 324
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-6

Query Match 88.6%; Score 1612; DB 4; Length 324;
Best Local Similarity 90.6%; Pred. No. 4.2e-164;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60

Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKPFVSEDDPVVKKIALREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Qy 121 NCIRDIPENILITKOGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYGS 180
Db 121 NCIRDIPENILITKOGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 240
Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 240
Qy 241 VASQSAGITGKLIPIRHOSIFKSNFFHGHSISPEPEMETLEEKFSVHPVAFNMKGCLK 300
Db 218 -----GKLIPIRHOSIFKSNFFHGHSISPEPEMETLEEKFSVHPVAFNMKGCLK 268
Qy 301 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOV 342
Db 269 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOV 310

RESULT 5
US-09-949-016-7552
; Sequence 7552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7552
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7552

Query Match 63.9%; Score 1162.5; DB 4; Length 367;
Best Local Similarity 63.8%; Pred. No. 7.7e-116;
Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;

Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKPFVSEDDPVVKKIALREIRMLKOLKH 60
Db 11 MEKYEKGIGEGSYGVVFKCRNRTGQIVAIKKFLESEDDPVVKKIALREIRMLKOLKH 70
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Db 71 PNLVNLIEVFRKRKMLHVFYCDHTLVHLDYRQGVPEHLVKSITWQTLQAVNFCCHK 130
Qy 121 NCIRDIPENILITKOGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYGS 179
Db 131 NCIRDIPENILITKHSVIKLCDFGFAELLTGSDYVTDYVATRWYRSPPELLVGDTOYG 190
Qy 180 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 191 PPVDVWAIGCVFAELLSGVPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 228
Qy 240 AVASQSAGITGKLIPIRHOSIFKSNFFHGHSISPEPEMETLEEKFSVHPVAFNMKGCL 299
Db 229 -----GDLIPRHQQVFTNQYFSGVKIPDPEDMEPELEKFPNISYPALGLLKGCL 278

Qy 300 KMPDDLRLTCSQLLESSYFDSFQEAQIKRKARNE 333
Db 279 HMDPTEBLTCEQLLHHPYFENIREIEDLAKEHKN 312

RESULT 6
US-09-411-628-11
; Sequence 11, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-628-11

Query Match 63.6%; Score 1157.5; DB 4; Length 358;
Best Local Similarity 64.7%; Pred. No. 2.6e-115;
Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;

Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKPFVSEDDPVVKKIALREIRMLKOLKH 60
Db 2 MEKYEKGIGEGSYGVVFKCRNRTGQIVAIKKFLESEDDPVVKKIALREIRMLKOLKH 61
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Db 62 PNLVNLIEVFRKRKMLHVFYCDHTLVHLDYRQGVPEHLVKSITWQTLQAVNFCCHK 121
Qy 121 NCIRDIPENILITKOGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYGS 179
Db 122 NCIRDIPENILITKHSVIKLCDFGFAELLTGSDYVTDYVATRWYRSPPELLVGDTOYG 181
Qy 180 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 219
Qy 240 AVASQSAGITGKLIPIRHOSIFKSNFFHGHSISPEPEMETLEEKFSVHPVAFNMKGCL 299
Db 220 -----GDLIPRHQQVFTNQYFSGVKIPDPEDMEPELEKFPNISYPALGLLKGCL 269
Qy 300 KMPDDLRLTCSQLLESSYFDSFQEAQ 325
Db 270 HMDPTEBLTCEQLLHHPYFENIREIE 295

RESULT 7
US-10-174-794-11
; Sequence 11, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11

LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-174-794-11

Query Match 63.6%; Score 1157.5; DB 4; Length 358;
Best Local Similarity 64.7%; Pred. No. 2.6e-115;
Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;

QY 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 2 MEKYEKIGKIGESYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 61
QY 61 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELRNPNAGVGVKSVLWQTLQALNFCCHI 120
DB 62 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELRNPNAGVGVKSVLWQTLQALNFCCHI 121
QY 121 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 179
DB 122 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 181
QY 180 SSVDIWAIGCVFAELLTGOPWPKSGDVLDYLIITLVTETGFRHVDQAGLELLTSSDPP 239
DB 182 PPVDVWAIGCVFAELLTGOPWPKSGDVLDYLIITLVTETGFRHVDQAGLELLTSSDPP 219
QY 240 AVASQAGITGKLIPIRHQSIKNSGFHGISIPEPEDEMETLEKFSVHPVALNFMKGCL 299
DB 220 -----GOLIPRHQSQVFSTNOVFGVKIPDPEDMELEKFPNISYPALGKLLKCL 269
QY 300 KNPDPDLTCSOLLESSYFDSQEAQ 325
DB 270 HMDPTERLTCEQLLHHHPYFENIREIE 295

RESULT 8

US-09-411-628-4
Sequence 4, Application US/09411628
Patent No. 6428994
GENERAL INFORMATION:
APPLICANT: University of Southern California
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
EARLIER APPLICATION NUMBER: 1999-10-01
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 566
TYPE: PRT
ORGANISM: Orcytolagus cuniculus
US-09-411-628-4

Query Match 51.7%; Score 941.5; DB 4; Length 566;
Best Local Similarity 49.7%; Pred. No. 7.4e-92;
Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;

QY 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MEKYEKIGKIGESYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELRNPNAGVGVKSVLWQTLQALNFCCHI 120
DB 61 ENLVNLIEVCKKRWLVFVFDHTLLDLEFPNGLDQVQVVKYLFQILINGIGFCHSH 120
QY 121 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 179
DB 121 NIHRDIKPENILVSGQVVKLCDFGFARTLAAPGEVYTDYVATRYRAPELLVGVKYG 180
QY 180 SSVDIWAIGCVFAELLTGOPWPKSGDVLDYLIITLVTETGFRHVDQAGLELLTSSDPP 239
DB 181 KAVDVWAIGCVFAELLTGOPWPKSGDVLDYLIITLVTETGFRHVDQAGLELLTSSDPP 218
QY 240 AVASQAGITGKLIPIRHQSIKNSGFHGISIPEPEDEMETLEKFSVHPVALNFMKGCL 299
DB 219 -----GNLIPRHQELFYKPNVFAVRLPEIKSESEPLERYPKLSEVVIDLAKKCL 268
QY 300 KNPDPDLTCSOLLESSYFDSF-----QEAQIK--RKARN-----EGRNRRQO 341
DB 269 HVDPDKRPFCAELLHHDFFQMDGFAERFSQBLQMKVQKDAENISLSKKSQNRKKEK 324

RESULT 10

US-09-949-016-7954
Sequence 7954, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016

QY 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MEKYEKIGKIGESYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRRKMLHVEYCDHTLLNELRNPNAGVGVKSVLWQTLQALNFCCHI 120
DB 61 ENLVNLIEVCKKRWLVFVFDHTLLDLEFPNGLDQVQVVKYLFQILINGIGFCHSH 120
QY 121 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 179
DB 121 NIHRDIKPENILVSGQVVKLCDFGFARTLAAPGEVYTDYVATRYRAPELLVGVKYG 180
QY 180 SSVDIWAIGCVFAELLTGOPWPKSGDVLDYLIITLVTETGFRHVDQAGLELLTSSDPP 239
DB 181 KAVDVWAIGCVFAELLTGOPWPKSGDVLDYLIITLVTETGFRHVDQAGLELLTSSDPP 218
QY 240 AVASQAGITGKLIPIRHQSIKNSGFHGISIPEPEDEMETLEKFSVHPVALNFMKGCL 299
DB 219 -----GNLIPRHQELFYKPNVFAVRLPEIKSESEPLERYPKLSEVVIDLAKKCL 268
QY 300 KNPDPDLTCSOLLESSYFDSF-----QEAQIK--RKARN-----EGRNRRQO 341
DB 269 HVDPDKRPFCAELLHHDFFQMDGFAERFSQBLQMKVQKDAENISLSKKSQNRKKEK 324

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7954
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Human
; ORGANISM: Homo sapiens
; US-09-949-016-7954

Query Match      50.3%; Score 915.5; DB 4; Length 475;
Best Local Similarity 48.3%; Pred. No. 3.4e-89;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
Db 3 MEKYNLGLVGECSYGMVMKCRNKDTGRIVAIAKKFLESDDDKVMVKIAMREIKLLKOLRH 62

Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 63 ENLVNLLEVCKKRWYLVFEVDHTLDDLEFPNGLDYQVQVKYLFQIINGIGFCHSH 122

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDYVATRWYRAPELLVGDVKYG 182

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 183 KAVDVWAIGCLVTEMFMGEPLFPFGSDSDIDQLYHMMCL----- 220

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEDMETLEKFSVDVHPVAFNMKGCL 299
Db 221 -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERYPKLSEVIDLAKKCL 270

Qy 300 KNMPDDLRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 271 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 326

RESULT 11
US-09-411-628-10
; Sequence 10, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
; US-09-411-628-10

Query Match      50.3%; Score 915.5; DB 4; Length 493;
Best Local Similarity 48.3%; Pred. No. 3.7e-89;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYNLGLVGECSYGMVMKCRNKDTGRIVAIAKKFLESDDDKVMVKIAMREIKLLKOLRH 60

Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 61 ENLVNLLEVCKKRWYLVFEVDHTLDDLEFPNGLDYQVQVKYLFQIINGIGFCHSH 120

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDYVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAIGCLVTEMFMGEPLFPFGSDSDIDQLYHMMCL----- 218

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEDMETLEKFSVDVHPVAFNMKGCL 299
Db 219 -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERYPKLSEVIDLAKKCL 268

Qy 300 KNMPDDLRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324
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Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 61 ENLVNLLEVCKKRWYLVFEVDHTLDDLEFPNGLDYQVQVKYLFQIINGIGFCHSH 120

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDYVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAIGCLVTEMFMGEPLFPFGSDSDIDQLYHMMCL----- 218

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEDMETLEKFSVDVHPVAFNMKGCL 299
Db 219 -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERYPKLSEVIDLAKKCL 268

Qy 300 KNMPDDLRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324

RESULT 12
US-10-174-794-10
; Sequence 10, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
; US-10-174-794-10

Query Match      50.3%; Score 915.5; DB 4; Length 493;
Best Local Similarity 48.3%; Pred. No. 3.7e-89;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYNLGLVGECSYGMVMKCRNKDTGRIVAIAKKFLESDDDKVMVKIAMREIKLLKOLRH 60

Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 61 ENLVNLLEVCKKRWYLVFEVDHTLDDLEFPNGLDYQVQVKYLFQIINGIGFCHSH 120

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDYVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAIGCLVTEMFMGEPLFPFGSDSDIDQLYHMMCL----- 218

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEDMETLEKFSVDVHPVAFNMKGCL 299
Db 219 -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERYPKLSEVIDLAKKCL 268

Qy 300 KNMPDDLRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324
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RESULT 13

US-09-671-050-2
 ; Sequence 2, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-2

Query Match 43.5%; Score 791; DB 4; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.8e-76;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60

QY 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADVIVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADVIVKSVLWQTLQALNFCIH 120

QY 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151
 DB 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151

RESULT 14

US-09-671-050-8
 ; Sequence 8, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-8

Query Match 43.5%; Score 791; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2e-76;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60

QY 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADVIVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADVIVKSVLWQTLQALNFCIH 120

QY 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151
 DB 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151

RESULT 15

US-09-538-092-1236
 ; Sequence 1236, Application US/09538092
 ; Patent No. 6753314
 ; GENERAL INFORMATION:
 ; APPLICANT: Giot, Loic
 ; APPLICANT: Mansfield, Traci A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966-542
 ; CURRENT APPLICATION NUMBER: US/09/538,092
 ; CURRENT FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/178,965
 ; PRIOR FILING DATE: 2000-02-01
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CurPatSeqFormatter Version 0.9
 ; SEQ ID NO 1236
 ; LENGTH: 305
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (0)..(0)
 ; OTHER INFORMATION: Polypeptide Accession Number Q00526
 ; US-09-538-092-1236

Query Match 31.0%; Score 565; DB 4; Length 305;
 Best Local Similarity 36.8%; Pred. No. 6.5e-52;
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QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFP---VESEDDPVVKKIALREIRMLKQ 57
 DB 1 MDMFQKEKIGEGTYGVVYKAKNRETGQLVALKIRLDLEMEGVP---STAIRISLLKE 57

QY 58 LKHPNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNNG-VADGVKSVLWQTLQALNF 116
 DB 58 LKHPNIVRLDDVVHNERKLYLVFEFLSQDLKXYMSTPGSELPHLIKSYLFLQLQGVSF 117

QY 117 CHIHNCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 175
 DB 118 CHSHRVIHRIKPNILITKQGIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 177

QY 176 TQGVSDIWAIGCVFAELLTGQPLWPKSDVDQLYLIRTLVETGFRHVDQAGLELTS 235
 DB 178 KYTTAVDIWISGICFAEMVTKALFPGDSEIDQLFRIFRML----- 219

QY 236 SDPPAVASQSA--GITGLIPRHQISFKNSGPFHGIGISPEPE-DMETLEKFSVDVHPVAL 292
 DB 220 ----GTPSEDTPGVT--QLPDYKGSF-----PKWTRKGLEEIVPNLEPGR 260

QY 293 NFMKGLKMNPDRLTCSQLLESYFDSFQRAQIKRK 329
 DB 261 DILMQLQLQDPSQRITAKTALAHYPFSSPEPSPARQ 297

Search completed: April 22, 2005, 06:52:56
 Job time : 36.071 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 06:50:50 ; Search time 859.637 Seconds
(without alignments)
134.334 Million cell updates/sec

Title: US-10-766-691-10

Perfect score: 1820

Sequence: 1 MEKYEKLAKTGEISYGVVFK.....RKARNEGRNRROOVLPKLS 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- Published Applications AA:*
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 - 3: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
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 - 5: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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 - 12: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
 - 13: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
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 - 20: /cgm2_6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1636	89.9	315	17	US-10-766-691-12
4	1613	88.6	342	15	US-10-333-314-10
5	1612	88.6	324	17	US-10-766-691-6
6	1162.5	63.9	358	15	US-10-363-616-391
7	1160.5	63.8	338	16	US-10-664-421-97
8	1157.5	63.6	358	14	US-10-174-794-11
9	1134	62.3	228	9	US-09-834-496A-2
10	941.5	51.7	566	14	US-10-174-794-4
11	915.5	50.3	493	14	US-10-174-794-10
12	915.5	50.3	493	15	US-10-369-022-22
13	915.5	50.3	493	16	US-10-757-262-108
					Sequence 10, Appl
					Sequence 4, Appl
					Sequence 12, Appl
					Sequence 10, Appl
					Sequence 6, Appl
					Sequence 391, Appl
					Sequence 97, Appl
					Sequence 11, Appl
					Sequence 2, Appl
					Sequence 4, Appl
					Sequence 10, Appl
					Sequence 42, Appl
					Sequence 108, Appl

14	791	43.5	187	17	US-10-766-691-2	Sequence 2, Appl
15	791	43.5	198	17	US-10-766-691-8	Sequence 8, Appl
16	758.5	41.7	455	16	US-10-620-052A-34	Sequence 34, Appl
17	712.5	39.1	154	16	US-10-250-889-62	Sequence 62, Appl
18	565	31.0	305	15	US-10-394-322A-8	Sequence 8, Appl
19	565	31.0	305	16	US-10-408-765A-544	Sequence 544, Appl
20	565	31.0	305	16	US-10-620-052A-20	Sequence 20, Appl
21	563	30.9	544	14	US-10-072-036-113	Sequence 113, Appl
22	557	30.6	298	9	US-09-771-161A-187	Sequence 187, Appl
23	557	30.6	544	14	US-10-072-036-115	Sequence 115, Appl
24	556	30.5	298	14	US-10-174-794-13	Sequence 27, Appl
25	556	30.5	298	14	US-10-295-681-27	Sequence 14, Appl
26	555	30.5	297	14	US-10-295-681-51	Sequence 51, Appl
27	554	30.4	298	11	US-09-969-034-4493	Sequence 4493, Appl
28	554	30.4	298	15	US-10-394-322A-7	Sequence 7, Appl
29	554	30.4	298	16	US-10-620-052A-55	Sequence 55, Appl
30	554	30.4	298	16	US-10-664-421-14	Sequence 14, Appl
31	554	30.4	298	16	US-10-664-421-51	Sequence 51, Appl
32	551.5	30.3	294	15	US-10-389-566-1333	Sequence 1333, Appl
33	551	30.3	294	15	US-10-334-143-181	Sequence 181, Appl
34	550	30.2	298	14	US-10-295-681-31	Sequence 31, Appl
35	550	30.2	298	14	US-10-295-681-39	Sequence 39, Appl
36	548	30.1	298	14	US-10-295-681-29	Sequence 29, Appl
37	548	30.1	298	14	US-10-295-681-43	Sequence 43, Appl
38	546.5	30.0	294	15	US-10-389-566-1030	Sequence 1030, Appl
39	546	30.0	298	14	US-10-295-681-35	Sequence 35, Appl
40	545.5	30.0	294	15	US-10-389-566-1087	Sequence 1087, Appl
41	545	29.9	297	14	US-10-060-065-11	Sequence 11, Appl
42	545	29.9	297	14	US-10-059-585-32	Sequence 32, Appl
43	545	29.9	297	14	US-10-177-293-41	Sequence 41, Appl
44	545	29.9	297	14	US-10-174-794-12	Sequence 12, Appl
45	545	29.9	297	14	US-10-204-041-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-10-766-691-10
; Sequence 10, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 347
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-10

Query Match 100.0%; Score 1820; DB 17; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.66-143;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKFFVESEDDPVVKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKFFVESEDDPVVKIALREIRMLKOLKH 60

QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
QY 121 NCIHRLDKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIHRLDKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
DB 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
QY 241 VASQAGITGKLIIPRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
DB 241 VASQAGITGKLIIPRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347
DB 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347

RESULT 2
US-10-766-691-4
; Sequence 4, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766.691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-4

Query Match 98.7%; Score 1796; DB 17; Length 356;
Best Local Similarity 100.0%; Pred. No. 3.7e-141;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
DB 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
QY 121 NCIHRLDKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIHRLDKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
DB 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
QY 241 VASQAGITGKLIIPRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
DB 241 VASQAGITGKLIIPRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300

QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 342
DB 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 342

RESULT 3
US-10-766-691-12
; Sequence 12, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766.691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 315
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-12

Query Match 89.9%; Score 1636; DB 17; Length 315;
Best Local Similarity 90.8%; Pred. No. 6.7e-128;
Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
DB 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
QY 121 NCIHRLDKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIHRLDKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
DB 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
QY 241 VASQAGITGKLIIPRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
DB 241 VASQAGITGKLIIPRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347
DB 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 315

RESULT 4
US-10-333-314-10
; Sequence 10, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.

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; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1698381CD1
US-10-333-314-10

Query Match      88.6%; Score 1613; DB 15; Length 342;
Best Local Similarity 89.9%; Pred. No. 6e-126;
Matches 312; Conservative 1; Mismatches 0; Indels 34; Gaps 2;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120

Qy 121 NCIRDIKPENILITKQIIKICDFGPAQLIPGDAYTDVYATWYRAPELLVGDTOYGS 180
Db 121 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120

Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240

Qy 241 VASOSAGITKGLIPRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300
Db 241 VASOSAGITKGLIPRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300

Qy 218 -----GKLI PRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268
Db 218 -----GKLI PRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268

Qy 301 MNPDDLTCQSLLSESYFDSFQEAQIKRKARNEGRRRRQV 345
Db 269 MNPDDLTCQSLLSESYFDSFQEAQIKRKARNEGRRRRQV 315

RESULT 5
US-10-766-691-6
; Sequence 6, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn

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; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 324
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-6

Query Match      88.6%; Score 1612; DB 17; Length 324;
Best Local Similarity 90.6%; Pred. No. 6.9e-126;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120

Qy 121 NCIRDIKPENILITKQIIKICDFGPAQLIPGDAYTDVYATWYRAPELLVGDTOYGS 180
Db 121 NCIRDIKPENILITKQIIKICDFGPAQLIPGDAYTDVYATWYRAPELLVGDTOYGS 180

Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240

Qy 241 VASOSAGITKGLIPRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300
Db 241 VASOSAGITKGLIPRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300

Qy 218 -----GKLI PRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268
Db 218 -----GKLI PRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268

Qy 301 MNPDDLTCQSLLSESYFDSFQEAQIKRKARNEGRRRRQV 342
Db 269 MNPDDLTCQSLLSESYFDSFQEAQIKRKARNEGRRRRQV 310

RESULT 6
US-10-363-616-391
; Sequence 391, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 391
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-391

Query Match      63.9%; Score 1162.5; DB 15; Length 358;
Best Local Similarity 63.8%; Pred. No. 2e-88;
Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

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Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQLKH 61
 Qy 61 PNLVNLLEVERRRKRMHLVFEYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI 120
 Db 62 PNLVNLLEVERRRKRMHLVFEYCDHTVLHEDRYQGVPEHLVKSITWOTLQAVNFCCHK 121
 Qy 121 NCIHRIKPENILITKGIKIICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDQY 179
 Db 122 NCIHROVKPENILITKHSVILKCLDFGARLLTGPSDYITDYATRWYRSPPELLVGDQY 181
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQLYLIRKTL----- 219
 Qy 240 AVASQAGITGKLI PRHQSIKSNFGFHGISIPEDMETLEKFSDVHPVAFNFMKGCL 299
 Db 220 -----GDLIPRHOQVFTNQYFSGVKIPDPEDMEPLKFPNISYPALGGLKGL 269
 Qy 300 KMPDRLTCSQLLESSYFDSFOEAQIKRKARNE 333
 Db 270 HMDPTERTLTCQQLLHHPYFENIRIEDLAKENK 303

RESULT 7

US-10-664-421-97
 ; Sequence 97, Application US/10664421
 ; Publication No. US20040142864A1
 ; GENERAL INFORMATION:

; APPLICANT: BREMER, RYAN
 ; APPLICANT: TIRAHIM, PRABHA
 ; APPLICANT: KOMAR, ABHINAV
 ; APPLICANT: MANDIYAN, VALSAN
 ; APPLICANT: MILBURN, MICHAEL V.
 ; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
 ; FILE REFERENCE: 039363/0703
 ; CURRENT APPLICATION NUMBER: US/10/664,421
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/412,341
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/411,398
 ; PRIOR FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 169
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 97
 ; LENGTH: 338
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-664-421-97

Query Match 63.8%; Score 1160.5; DB 16; Length 338;
 Best Local Similarity 63.8%; Pred. No. 2.8e-88;
 Matches 213; Conservative 41; Mismatches 47; Indels 33; Gaps 2;

Qy 1 MEKYEKIAKTGEGSYGVVFKCRNKTSGQVAVKKFVSEDDPVYKVKIALREIRMLKQLKH 60
 Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQLKH 61
 Qy 61 PNLVNLLEVERRRKRMHLVFEYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI 120
 Db 62 PNLVNLLEVERRRKRMHLVFEYCDHTVLHEDRYQGVPEHLVKSITWOTLQAVNFCCHK 121
 Qy 121 NCIHRIKPENILITKGIKIICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDQY 179
 Db 122 NCIHROVKPENILITKHSVILKCLDFGARLLTGPSDYITDYATRWYRSPPELLVGDQY 181
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQLYLIRKTL----- 219
 Qy 240 AVASQAGITGKLI PRHQSIKSNFGFHGISIPEDMETLEKFSDVHPVAFNFMKGCL 299
 Db 220 -----GDLIPRHOQVFTNQYFSGVKIPDPEDMEPLKFPNISYPALGGLKGL 269

Qy 300 KMPDRLTCSQLLESSYFDSFOEAQIKRKARNE 333
 Db 270 HMDPTERTLTCQQLLHHPYFENIRIEDLAKENK 303

RESULT 8

US-10-174-794-11
 ; Sequence 11, Application US/10174794
 ; Publication No. US20030166220A1
 ; GENERAL INFORMATION:

; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: cDNA, GENOMIC, AND PREDICTED PROTEIN
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/10/174,794
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US/09/411,628
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: US 60/102,906
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-174-794-11

Query Match 63.6%; Score 1157.5; DB 14; Length 358;
 Best Local Similarity 64.7%; Pred. No. 5.2e-88;
 Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;

Qy 1 MEKYEKIAKTGEGSYGVVFKCRNKTSGQVAVKKFVSEDDPVYKVKIALREIRMLKQLKH 60
 Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQLKH 61
 Qy 61 PNLVNLLEVERRRKRMHLVFEYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI 120
 Db 62 PNLVNLLEVERRRKRMHLVFEYCDHTVLHEDRYQGVPEHLVKSITWOTLQAVNFCCHK 121
 Qy 121 NCIHRIKPENILITKGIKIICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDQY 179
 Db 122 NCIHROVKPENILITKHSVILKCLDFGARLLTGPSDYITDYATRWYRSPPELLVGDQY 181
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQLYLIRKTL----- 219
 Qy 240 AVASQAGITGKLI PRHQSIKSNFGFHGISIPEDMETLEKFSDVHPVAFNFMKGCL 299
 Db 220 -----GDLIPRHOQVFTNQYFSGVKIPDPEDMEPLKFPNISYPALGGLKGL 269

RESULT 9

US-09-834-496A-2
 ; Sequence 2, Application US/09834496A
 ; Patent No. US20020090701A1
 ; GENERAL INFORMATION:

; APPLICANT: Kapeller-Libermann
 ; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
 ; FILE REFERENCE: 381552000900
 ; CURRENT APPLICATION NUMBER: US/09/834,496A
 ; CURRENT FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/196,910
 ; PRIOR FILING DATE: 2000-04-13
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2

Qy LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-496A-2

Query Match 62.3%; Score 1134; DB 9; Length 228;
Best Local Similarity 98.2%; Pred. No. 2.8e-86;
Matches 213; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Db 1 MGKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNVGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNVGVADGVKSVLWQTLQALNFCCHI 120
Qy 121 NCIRHDIKPENILITKOGIHKICDFGAQILIPGDATYDVATRWYRAPELLVGDTOYGS 180
Db 121 NCIRHDIKPENILITKOGIHKICDFGAQILIPGDATYDVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTQGPLWPKGSDVDQLYLIIRTL 217
Db 181 SVDIWAIGCVFAELLTQGPLWPKGSDVDQLYLIIRTL 217

RESULT 10
US-10-174-794-4
; Sequence 4, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-174-794-4

Query Match 51.7%; Score 941.5; DB 14; Length 566;
Best Local Similarity 49.7%; Pred. No. 8.7e-70;
Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;
Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNVGVADGVKSVLWQTLQALNFCCHI 120
Db 61 ENLVNLIEVCKKRWLYFEFVDHTILDLELFPNGLDQVQKYLFIINGIGFCHSH 120
Qy 121 NCIRHDIKPENILITKOGIHKICDFGAQILIPGDATYDVATRWYRAPELLVGDTOYG 179
Db 121 NCIRHDIKPENILITKOGIHKICDFGAQILIPGDATYDVATRWYRAPELLVGDTOYG 180
Qy 180 SVDIWAIGCVFAELLTQGPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVAIGCLVTEMFMEGPELFPDSDIDQLXHMCL----- 218
Qy 240 AVASQAGITCKLIPRHSIFKSNPFHGSIPEPEMETLEKFSVDVHPVAFNMKGCL 299
Db 219 -----GNLIPRHOELFKNPVFAGVRLPEIKEREPLRRYPKLSKVSEVVIDLAKKCL 268

Qy 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HVPDPKRPFCALLHDDFFQMDGFAERFSQELQKVKQDARNISLSKKSQNRKKEK 324
RESULT 11
US-10-174-794-10
; Sequence 10, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-10

Query Match 50.3%; Score 915.5; DB 14; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;
Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNVGVADGVKSVLWQTLQALNFCCHI 120
Db 61 ENLVNLIEVCKKRWLYFEFVDHTILDLELFPNGLDQVQKYLFIINGIGFCHSH 120
Qy 121 NCIRHDIKPENILITKOGIHKICDFGAQILIPGDATYDVATRWYRAPELLVGDTOYG 179
Db 121 NCIRHDIKPENILITKOGIHKICDFGAQILIPGDATYDVATRWYRAPELLVGDTOYG 180
Qy 180 SVDIWAIGCVFAELLTQGPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVAIGCLVTEMFMEGPELFPDSDIDQLXHMCL----- 218
Qy 240 AVASQAGITCKLIPRHSIFKSNPFHGSIPEPEMETLEKFSVDVHPVAFNMKGCL 299
Db 219 -----GNLIPRHOELFKNPVFAGVRLPEIKEREPLRRYPKLSKVSEVVIDLAKKCL 268
Qy 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HVPDPKRPFCALLHDDFFQMDGFAERFSQELQKVKQDARNISLSKKSQNRKKEK 324

RESULT 12
US-10-369-022-22
; Sequence 22, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44372,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MF102-027PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/369,022

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; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/387,536
; PRIOR FILING DATE: 2002-06-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-022-22

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Query Match      50.3%; Score 915.5; DB 15; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

QY 1 MEKYEKLAKTGGSGYGVFKCRNKTSGQVAVKVFVESEDDPVVKJALREIMLKQKH 60
Db 1 MEKYENLGLVGGSGYGVFKCRNKTGRIVAKKFLFESDDDDKMKVKIAMREIKLKQKH 60
QY 61 PNLVNLIEVFRKRKHVLFVEYCDHTLLNELRNPNGVADGVKISVLWQTLQALNFCCHI 120
Db 61 ENLVNLLEVCCKRWYLVFEVDHTLDDLELFPNGLDYQVQVKYLFQIINGIGFCHSH 120
QY 121 NCIRHDIKPENILITKQGIKICDPGFAOIL-IPGDATDVVATRWYRAPELLVGTQYG 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFAITLAAPGEVYTDVATRWYRAPELLVGDYKYG 180
QY 180 SSVDIWAICGVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAICGLVTEMFMGEPFLFGSDSDIDQLYHMMCL-----218
QY 240 AVASQAGITGKLIPIRHQSIFKSNGFHGISIPEDMETLEKFSVHPVVALNFMKGL 299
Db 219 -----GNLIPRHOELFNKNPVFAGVRLPEIKEREPLERYPKLSEVIDLAKKCL 268
QY 300 KMNPDRLTCSQLLESSYF--DSF-----OEAQIK--RKARN-----EGNRNRQO 341
Db 269 HIDPKRPFCAELLHHDFQMDGFAERFSQELQLKVQKDARNVLSKSKSNRKKK 324

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RESULT 13

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US-10-757-262-108
; Sequence 108, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22445, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,

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RESULT 14

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US-10-766-691-2
; Sequence 2, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn

```

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; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-108

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```

Query Match      50.3%; Score 915.5; DB 16; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

QY 1 MEKYEKLAKTGGSGYGVFKCRNKTSGQVAVKVFVESEDDPVVKJALREIMLKQKH 60
Db 1 MEKYENLGLVGGSGYGVFKCRNKTGRIVAKKFLFESDDDDKMKVKIAMREIKLKQKH 60
QY 61 PNLVNLIEVFRKRKHVLFVEYCDHTLLNELRNPNGVADGVKISVLWQTLQALNFCCHI 120
Db 61 ENLVNLLEVCCKRWYLVFEVDHTLDDLELFPNGLDYQVQVKYLFQIINGIGFCHSH 120
QY 121 NCIRHDIKPENILITKQGIKICDPGFAOIL-IPGDATDVVATRWYRAPELLVGTQYG 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFAITLAAPGEVYTDVATRWYRAPELLVGDYKYG 180
QY 180 SSVDIWAICGVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAICGLVTEMFMGEPFLFGSDSDIDQLYHMMCL-----218
QY 240 AVASQAGITGKLIPIRHQSIFKSNGFHGISIPEDMETLEKFSVHPVVALNFMKGL 299
Db 219 -----GNLIPRHOELFNKNPVFAGVRLPEIKEREPLERYPKLSEVIDLAKKCL 268
QY 300 KMNPDRLTCSQLLESSYF--DSF-----OEAQIK--RKARN-----EGNRNRQO 341
Db 269 HIDPKRPFCAELLHHDFQMDGFAERFSQELQLKVQKDARNVLSKSKSNRKKK 324

```

; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US-0046-USA
 ; CURRENT FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-766-691-2

Query Match 43.5%; Score 791; DB 17; Length 187;
 Best Local Similarity 100.0%; Pred. No. 7.7e-58;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVSEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVSEDDPVVKKIALREIRMLKQLKH 60
 Qy 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
 Db 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
 Qy 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151
 Db 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151

RESULT 15
 US-10-766-691-8
 ; Sequence 8, Application US/10766691
 ; Publication No. US20050042626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/766,691
 ; CURRENT FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-766-691-8

Query Match 43.5%; Score 791; DB 17; Length 198;
 Best Local Similarity 100.0%; Pred. No. 8.3e-58;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVSEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVSEDDPVVKKIALREIRMLKQLKH 60
 Qy 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120

Db 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
 Qy 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151
 Db 121 NCIHRIKPNILITKQGIKICDFGFAQIL 151

Search completed: April 22, 2005, 07:36:42
 Job time : 860.637 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2005, 03:32:53 ; Search time 28.3051 Seconds
(without alignments)
1179.546 Million cell updates/sec

Title: US-10-766-691-10
Perfect score: 1820
Sequence: 1 MEKYEKLAKTGEISYGVVFK.....RKARNEGRRRRQVLPKLS 347
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1157.5	63.6	358	2 S23383	protein kinase (EC
2	1149.5	63.2	376	2 S22745	serine/threonine p
3	565	31.0	305	2 S23382	protein kinase (EC
4	563	30.9	302	1 I50474	protein kinase (EC
5	558.5	30.7	292	2 S40021	protein kinase (EC
6	555	30.5	297	2 A37871	protein kinase (EC
7	554	30.4	298	2 A41227	protein kinase (EC
8	552.5	30.4	294	2 B40444	protein kinase (EC
9	551.5	30.3	294	2 S22440	protein kinase (EC
10	551.5	30.3	294	2 S23095	protein kinase (EC
11	546.5	30.0	294	2 A40444	protein kinase (EC
12	546.5	30.0	294	2 T49271	CELL DIVISION CONT
13	545	29.9	297	2 A29539	protein kinase (EC
14	545	29.9	298	1 A44878	protein kinase (EC
15	542	29.8	297	1 I45977	cyclin-dependent k
16	541	29.7	297	1 S24913	protein kinase (EC
17	540.5	29.7	297	1 S12009	protein kinase cdc
18	540.5	29.7	302	2 B43439	protein kinase (EC
19	540	29.7	302	2 A44349	protein kinase (EC
20	539	29.6	303	1 S06011	protein kinase (EC
21	537	29.5	288	1 S42566	protein kinase (EC
22	536.5	29.5	311	2 S36619	protein kinase (EC
23	535.5	29.4	294	1 S19728	protein kinase (EC
24	535.5	29.4	294	1 J02243	protein kinase (EC
25	535.5	29.4	294	1 S42049	protein kinase (EC
26	532	29.2	301	1 S19209	protein kinase (EC
27	531	29.2	292	1 A46365	protein kinase (EC
28	530.5	29.1	294	2 S31332	protein kinase (EC
29	529	29.1	292	1 A45091	protein kinase (EC

30	529	29.1	292	1 I49592	protein kinase (EC
31	527.5	29.0	308	1 S53538	protein kinase (EC
32	527	29.0	297	1 A36074	protein kinase (EC
33	527	29.0	301	1 S42101	protein kinase (EC
34	526.5	28.9	291	2 S23386	protein kinase (EC
35	526	28.9	293	2 J50374	cyclin-dependent k
36	526	28.9	294	2 S51008	protein kinase (EC
37	526	28.9	296	2 S24386	protein kinase (EC
38	524	28.8	302	1 OKBY85	protein kinase PHO
39	521.5	28.7	302	2 T17115	protein kinase cdc
40	519.5	28.5	346	2 A54820	CDK-activating pro
41	518	28.5	292	2 S22441	protein kinase (EC
42	517.5	28.4	346	2 A56231	MOL5/CDK-activatin
43	516.5	28.4	314	1 S12007	protein kinase (EC
44	514	28.2	293	2 T02922	protein kinase (EC
45	514	28.2	346	1 I78840	protein kinase (EC

ALIGNMENTS

RESULT 1

S23383
protein kinase (EC 2.7.1.37) cdc2-related KKIALRE - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: S23383; S22744
R;Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai
EMBO J. 11, 2909-2917, 1992
A;Title: A family of human cdc2-related protein kinases.
A;Reference number: S23382; MUID:92347325; PMID:1639063
A;Accession: S23383
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-358 <MEY>
A;Cross-references: UNIPROT:Q00532; EMBL:X66358; NID:g36614; PIDN:CAA47002.1; PID:g36615
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;3-278/Domain: protein kinase homology <KIN>
F;11-19/Region: protein kinase ATP-binding motif
F;34,52,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 63.6%; Score 1157.5; DB 2; Length 358;
Best Local Similarity 64.7%; Pred. No. 2.4e-45;
Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;

Qy	1	MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKQLKH	60
Db	2	MEKYEKLGKIGEGSYGVVFKCRNRTDQIVAKKFLSEDDPVIKIALREIRMLKQLKH	61
Qy	61	PNLVNLLIEVFRKRKMLHVFYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH	120
Db	62	PNLVNLLIEVFRKRKRLHLVFYCDHTVLHLDLRYQGVPEHLVKSITWQTLQAVNFCKH	121
Qy	121	NCIHRDKPENILITKQGIKICDFGFAQLI-PCDAYTDYVATRWYRAPELLVGDQYQ	179
Db	122	NCIHRDKPENILITKHSVKLCDFGFARLLTGSDYYTDYVATRWYRSPELLVGDQYQ	181
Qy	180	SSVDIWAIGCVFALLTGQPLWPKGSVDVQLYLIRTLVETGFRHVDQAGLELLTSSDPP	239
Db	182	PPVDVWAIGCVFALLSGVPLWPKGSVDVQLYLIRKTL-----	219
Qy	240	AVASQSGAGITKGLIPRHQSIFKSNGFPHGISIPEDMETLEEKFSVDVHPVALNFMKGL	299
Db	220	-----GDLIPRQVQVFTNQYFSGVKIPDPEDMEPLEKFPNISYPALGLLKGL	269
Qy	300	KMNPDRLTCSLLESYFDSFQEAQ	325
Db	270	HMDPTERTLCEQLLHHPYFENIREIE	295

RESULT 2

S22745

serine/threonine protein kinase KIALRE (EC 2.7.1.1) - human
 C:Species: Homo sapiens (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997
 C:Accession: S22745
 R:Meyerson, M.L.
 submitted to the EMBL Data Library, May 1992
 A:Reference number: S22743
 A:Accession: S22745
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-376 <MEY>
 A:Cross-references: EMBL:X66359
 C:Genetics:
 A:Introns: 152/3; 170/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F;3-296/Domain: protein kinase homology <KIN>
 F;11-19/Region: protein kinase ATP-binding motif

Query Match 63.2%; Score 1149.5; DB 2; Length 376;
 Best Local Similarity 61.3%; Pred. No. 5.7e-45; Indels 51; Gaps 2;
 Matches 211; Conservative 41; Mismatches 41

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
 DB 2 MEKYEKIGKIGESYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 61
 QY 61 PNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFC 120
 DB 62 PNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFC 121
 QY 121 NCIRHDKPENILITKOGIIKICDFGFAQIL-----PGDAYTDYV 161
 DB 122 NCIRHDKPENILITKOGIIKICDFGFAQILFXFQPSAAVFCPSITGXTGSPDYDYV 181
 QY 162 ATRWYRAPELLVGTQYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTLVETG 221
 DB 182 ATRWYRPELLVGTQYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTLVETG 237
 QY 222 FRHVDQAGLELLTSSDPPAVASQASGITKGLIPHQSIKSNFFHGSIPEPEDMETLE 281
 DB 238 -----GDLIRHQVQVFTNQYFSGVKIPDPDEMPLE 269
 QY 282 EKFSDDVHPVAFNMKGLKMPDRLTCSQLLESSYFDSFOEAQ 325
 DB 270 LKPNISYPALGULLKGLHMDPTERLICEQLLHPYENIREIE 313

RESULT 3
 S23382
 protein kinase (EC 2.7.1.37) cdk3 - human
 C:Species: Homo sapiens (man)
 C>Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 09-Jul-2004
 C:Accession: S23382; S22743
 R:Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai
 EMBO J. 11, 2909-2917, 1992
 A:Title: A family of human cdc2-related protein kinases.
 A:Reference number: S23382; MUID:92347325; PMID:1639063
 A:Accession: S23382
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-305 <MEY>
 A:Cross-references: UNIPROT:Q00526; EMBL:X66357; NID:G36612; PID:G36613
 C:Genetics:
 A:Gene: GDB:CDK3
 A:Cross-references: GDB:283456
 A:Map position: 12q13-12q13
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F;2-255/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 31.0%; Score 565; DB 2; Length 305;
 Best Local Similarity 36.8%; Pred. No. 5.5e-19;
 Matches 124; Conservative 66; Mismatches 99; Indels 48; Gaps 9;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQ 57
 DB 1 MDMFQKVEKIGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQ 57
 QY 58 LKHPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFC 116
 DB 58 LKHPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFC 117
 QY 117 CHIHNCIHRDIPENILITKOGIIKICDFGFAQIL-----IPGDAYTDYVATRWYRAPELLVGD 175
 DB 118 CHSRVIRHDLKQONLLINELGAIKLADGLARAFGLVPLRTYTHEVVTLYRAPELLVGD 177
 QY 176 TOYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLT 235
 DB 178 KFTVTAVDIWSIGICFAEMVTRKALFGDSEIDQLFRFML----- 219
 QY 236 SDPPAVASQSA--GITKGLIPHQSIKSNFFHGSIPEPE-DMETLEBKFSDDVHPVAL 292
 DB 220 -----GTPSEDTPGVT--QLPDYKGSF-----PKWTRKGLLEEIVPNLEPEGR 260
 QY 293 NFMKGCGLKMPDRLTCSQLLESSYFDSFOEAQIKRK 329
 DB 261 DLMQLLOLDPSORITAKTALAHYPSSPEPSAARQ 297

RESULT 4
 I50474
 protein kinase (EC 2.7.1.37) cdc2 [similarity] - goldfish
 C:Species: Carassius auratus (goldfish)
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: I50474
 R:Kajiura, H.; Yamashita, M.; Katsu, Y.; Nagahama, Y.
 Dev. Growth Differ. 35, 647-654, 1993
 A:Title: Isolation and characterization of goldfish cdc2, a catalytic component of mature
 A:Reference number: I50474
 A:Accession: I50474
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-302 <RAJ>
 A:Cross-references: UNIPROT:P51958; GB:D17758; NID:G471097; PID:BA04605.1; PID:G471098
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F;2-256/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.9%; Score 563; DB 1; Length 302;
 Best Local Similarity 41.2%; Pred. No. 6.7e-19;
 Matches 117; Conservative 60; Mismatches 71; Indels 36; Gaps 6;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQ 59
 DB 1 MDDYLIKIEKIGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQ 59
 QY 60 HPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFC 117
 DB 60 HPNVRLDLVLMQESKLYLVFEFLSMDLKLYLDSIPSGQFMDPMLVKSLYLQLEGILFC 119
 QY 118 HIHNCIHRDIPENILITKOGIIKICDFGFAQIL-----IPGDAYTDYVATRWYRAPELLVGD 176
 DB 120 HCRVIRHDLKQONLLINELGAIKLADGLARAFGLVPLRTYTHEVVTLYRAPELLVGD 179
 QY 177 QYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTL----- 217
 DB 180 RYSTPVDVMSIGITFAELATKKPLFGHSDSEIDQLFRITLGTPTNNEVWDVESLPDYKN 239
 QY 218 -----VETGFRHVDQAGLELLTSS---DPPAVASQASGIT 249
 DB 240 TFPKWSGNLASTVKNLDKNGIDLLTKMLIYDPPKRIARQAMT 283

RESULT 5

S40021
protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum)
C/Species: Dictyostelium discoideum
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S40021; S39071
R/Michaelis, C.E.; Weeks, G.
A/Description: The unicellular organism Dictyostelium discoideum possesses a highly related protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum) submitted to the EMBL Data Library, August 1992
A/Reference number: S40021
A/Accession: S40021
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-292 <MIC>
A/Cross-references: UNIPROT:P34117; EMBL:L00652; NID:g167695; PIDN:AAA16056.1; PID:g167695
R/Michaelis, C.; Weeks, G.
Biochim. Biophys. Acta 1179, 117-124, 1993
A/Title: The isolation from a unicellular organism, Dictyostelium discoideum, of a highly related protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum) submitted to the EMBL Data Library, August 1992
A/Reference number: S39071; MUID:94032415; PMID:8218353
A/Accession: S39071
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-18, 'Y', 20-188, 'G', 190-292 <MI2>
A/Cross-references: EMBL:L00652
C/Complex: In various organisms, cdc2 has been identified as a component of the M-phase C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonine F/2-254/Domain: protein kinase homology <KIN>
F/10-18/Region: protein kinase ATP-binding motif
F/33,51,126,128/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.7%; Score 558.5; DB 2; Length 292;
Best Local Similarity 35.0%; Pred. No. 1e-18;
Matches 115; Conservative 66; Mismatches 101; Indels 47; Gaps 6;
Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLVEFRKKRMLVPEYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 120
Db 61 PNLVNLVEFRKKRMLVPEYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 120
Qy 121 NCIRHDKPENILITKQGIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOY 179
Db 121 RVLRDLKPQNLINRKGELKADFGARAFIPVITYSHEVVTWYRAPELLVGDTOY 180
Qy 180 SSVDIWAIGCVFAELLTGQPLMPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 TPDIWSALCIFAEMASGRPLFGSGTSDQLFRIFKILGTP-----NEESWP 227
Qy 240 AVASQSGITKGLIPRHOSIF-----KNSGFFHGISIPEDEMETLEKFSVHPVALN 293
Db 228 SITE-----LFYKTFDFVHPAHLSSIVHG-----LDEK-----GLN 260
Qy 294 FMKGLKWNPDRLTCSQLLESSYFDSFO 322
Db 261 LLSKWLQYDPNQRTAAALAKHPFDGLE 289

RESULT 6

A37871
protein kinase (EC 2.7.1.37) cdk2 - African clawed frog
N/Alternate names: cell division control protein CDC2 homolog Egl
C/Species: Xenopus laevis (African clawed frog)
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C/Accession: A37871; S15866; I51662; S14410
R/Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camonis, J.; Mac
Proc. Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991
A/Title: Cloning by differential screening of a Xenopus cDNA coding for a protein highly related to the cdc2 homolog - African clawed frog (Xenopus laevis) submitted to the EMBL Data Library, August 1991
A/Reference number: A37871; MUID:91126051; PMID:1704128

A/Accession: A37871
A/Molecule type: mRNA
A/Residues: 1-297 <PAR>
A/Cross-references: UNIPROT:P23437; UNIPROT:Q9PSU0; GB:X14227
R/le Guellec, R.
submitted to the EMBL Data Library, January 1989
A/Reference number: S15866
A/Accession: S15866
A/Molecule type: mRNA
A/Residues: 1-92, 'R', 94-297 <LEA>
A/Cross-references: EMBL:X14227; NID:g64665; PIDN:CAA32443.1; PID:g64666
R/Olive, M.; Theze, N.; Philippe, M.; Le Pennec, J.P.; Lerivray, H.
Gene 151, 81-88, 1994
A/Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in oocytes
A/Reference number: I51662; MUID:95129896; PMID:7828909
A/Accession: I51662
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-39 <OLI>
A/Cross-references: EMBL:U07979; NID:g473584; PIDN:AAA82123.1; PID:g473585
C/Genetics:
A/Gene: cdk2

C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F/2-255/Domain: protein kinase homology <KIN>
F/10-18/Region: protein kinase ATP-binding motif
F/33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.5%; Score 555; DB 2; Length 297;
Best Local Similarity 37.8%; Pred. No. 1.5e-18;
Matches 115; Conservative 59; Mismatches 90; Indels 40; Gaps 6;
Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MENFQKVEKIGEGTYGVVYKARNRETGEIVALKIRLDTETEGVPSTAIRSILKELNH 60
Qy 61 PNLVNLVEFRKKRMLVPEYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 119
Db 61 PNLVNLVEFRKKRMLVPEYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 120
Qy 120 HNCIRHDKPENILITKQGIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOY 178
Db 121 HRVLRDLKPQNLINRKGELKADFGARAFIPVITYSHEVVTWYRAPELLVGDTOY 180
Qy 179 GSSVDIWAIGCVFAELLTGQPLMPGKSDVDQLYLIIRTL----- 217
Db 181 STAVDIWSALCIFAEMITRRALPGDSEIDQLFRITLGTDPDSVWPGVTTMPDYKSTF 240
Qy 218 ---VETGFRHV-----DOAGLELLTSSDPPAVASOSAGITKGLIPRHOSIFKNSGFFHGIS 270
Db 241 PKWIRQDFSKVVPPLDEGRDLAQM---LOYDSNKRISAKVALTTP-----FFRDVS 290
Qy 271 IPEP 274
Db 291 RPTP 294

RESULT 7

A41227
protein kinase (EC 2.7.1.37) cdk2 - human
N/Alternate names: Egl homolog; protein kinase p34
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: A41227; S17873; S16520
R/Ninomiya-Tsuji, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K.
Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
A/Title: Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a
A/Reference number: A41227; MUID:92020980; PMID:1717994
A/Accession: A41227
A/Molecule type: mRNA

A/Residues: 1-298 <NIN>
A/Cross-references: UNIPROT:P24941; GB:M68520; NID:g180177; PIDN:AAA35667.1; PID:g180178
R/Tsai, L.H.; Harlow, E.; Meyerson, M.

Nature 353, 174-177, 1991
A;Title: Isolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-
A;Reference number: S17873; MUID:91367262; PMID:1653904
A;Accession: S17873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <TGA>
A;Cross-references: GB:X62071; NID:g312802; PIDN:CAA43985.1; PID:g312803
R;Elledge, S.J.; Spottswood, M.R.
EMBO J. 10, 2653-2659, 1991
A;Title: A new human p34 protein kinase, CDK2, identified by complementation of a cdc28
A;Reference number: S16520; MUID:91330891; PMID:1714386
A;Accession: S16520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-176, 'S', 178-298 <ELL>
A;Cross-references: EMBL:X61622; NID:g29848; PIDN:CAA43807.1; PID:g29849
C;Genetics:
A;Gene: GDB:CDK2
A;Cross-references: GDB:128984; OMIM:116953
A;Map position: 12q13-12q13
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-255/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;14,160/Binding site: phosphate (Thr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.4%; Score 554; DB 2; Length 298;
Best Local Similarity 38.4%; Pred. No. 1.7e-18;
Matches 118; Conservative 54; Mismatches 89; Indels 46; Gaps 6;
QY 1 MEKYELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
DB 1 MENFQKEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETGVPSTAIRISILLKELNH 60
QY 61 PNLVNLIEVFRKRKMHLEVEYCDHTLLN-NGVADGVTKSVLWOTLQALNFCI 119
DB 61 PNLVLLDVHTENKLVLEFHLQDLKPFMDASALTGIPLKISLVFQLQLQAFCHS 120
QY 120 HNCIHRDIPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGTQY 178
DB 121 HRVLRDLKPNLLINTEGAIKLADFLARAFGVVVRTYTHEVVTWYRAPELLGCKY 180
QY 179 GSSVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTL----- 217
DB 181 STAVDIWSLGCIFAEWVTRRALPFGDSEIDQLFRIFRTLGPDEVWVPGVTSMPDYKPSF 240
QY 218 ---VETGFRHV---DQAGLELTSS---DPPAVASQSAGITGKLIPIRHSQIFKSNQFFH 267
DB 241 PKWARQDFSKVVPVLDDEGRSLLSQMLHYDPNKRISAKAAL-----AHPPFQ 287
QY 268 GISIPEP 274
DB 288 DVTKPVP 294
RESULT 8
B40444
protein kinase (EC 2.7.1.37) cdc2 homolog B - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 28-Feb-1997
C;Accession: B40444
R;Colasanti, J.; Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A;Title: Isolation and characterization of cDNA clones encoding a functional p34 (cdc2) H
A;Reference number: A40444; MUID:91195354; PMID:2014258
A;Accession: B40444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-294 <COL>
A;Cross-references: GB:M60526

C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.4%; Score 552.5; DB 2; Length 294;
Best Local Similarity 35.4%; Pred. No. 1.9e-18;
Matches 119; Conservative 66; Mismatches 98; Indels 53; Gaps 9;
QY 1 MEKYELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
DB 1 MEQYKEKIGEGTYGVVYKALDKTANETIALKKIRLEQDEGVSPSTAIRISILLKEMNH 60
QY 61 PNLVNLIEVFRKRKMHLEVEYCDHTLLN-----ELERNPVGADVIVKSVLWOTLQAL 114
DB 61 GNIVLRHDVHSEKRIYLVFEYLDLKKPFMDSCPEFAKNPT-----LIKSYLYQILRGV 115
QY 115 NFIHNCIHRDIPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELL 172
DB 116 AYCHSHRVLRDLKPNLLIDRRNALKLADFLARAFGIPVTFTHVVTWYRAPELL 175
QY 173 VGDYQYSSVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTL---VETGFRHVDQAG 229
DB 176 LGARQYSTPVDVMSVGCIFAEWVNRKPLFPDSEIDELFKIFRVLGTPNEQGW----- 228
QY 230 LELLTSSDPPAVASQSAGITGKLIPIRHSQIFKSNQFFHGISIPEPEMETLEEKFSVDHP 289
DB 229 -----PGVSCLPDFKTA--FPRWQA-----QDLATI---VPLNEP 258
QY 290 VALNFMKGCILKMPDDRLTCSQLLESYFDSFOBAQ 325
DB 259 AGDLLLSKMLRYEFSKRIITARQALEHYFKDLEWVQ 294
RESULT 9
S22440
protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice
C;Species: Oryza sativa (rice)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S22440
R;Hashimoto, J.; Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Utsugi, Y.
Mol. Gen. Genet. 233, 10-16, 1992
A;Title: Isolation and characterization of cDNA clones encoding cdc2 homologues from Oryz
A;Reference number: S22440; MUID:92293101; PMID:1376401
A;Accession: S22440
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <HAS>
C;Cross-references: UNIPROT:P29618; EMBL:X60374; NID:g20342; PIDN:CAA42922.1; PID:g20343
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.3%; Score 551.5; DB 2; Length 294;
Best Local Similarity 34.8%; Pred. No. 2.2e-18;
Matches 116; Conservative 68; Mismatches 102; Indels 47; Gaps 8;
QY 1 MEKYELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
DB 1 MEQYKEKIGEGTYGVVYKARDKVTNETIALKKIRLEQDEGVSPSTAIRISILLKEMNH 60
QY 61 PNLVNLIEVFRKRKMHLEVEYCDHTLLN-----ELERNPVGADVIVKSVLWOTLQAL 114
DB 61 GNIVLRHDVHSEKRIYLVFEYLDLKKPFMDSCPEFAKNPT-----LIKSYLYQILRGV 115
QY 115 NFIHNCIHRDIPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELL 172
DB 116 AYCHSHRVLRDLKPNLLIDRRNALKLADFLARAFGIPVTFTHVVTWYRAPELL 175
QY 173 VGDYQYSSVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLE 232


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Db 176 LGSQYSTPVDVMSVGCIFAEWVQKPLFPDSEIDELFKIFRVLGTP----- 223
Qy 233 LTSDPPAVASQASGAGITCKLIPRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVAL 292
Db 224 -NEQSWFCVSS-----LPDYKSAPFK-----WQAQDLATI---VPTLDPAGL 261
Qy 293 NFMKGCLMNPDDRLTCSQLLESSYFDSFQEAQ 325
Db 262 DLLSKMLRYENPKRITARQALEHEYFKDLEWVQ 294

RESULT 10
protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana
N;Alternate names: cdc2 protein homolog; CDC2a protein; cell division control protein 2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S23095; A48984; JQ1337; JQ0967; S18202
R;Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.
FEBS Lett. 304, 73-77, 1992
A;Title: Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a
A;Reference number: S23095; MUID:92316202; PMID:1618302
A;Accession: S23095
A;Molecule type: DNA
A;Residues: 1-294 <INP>
A;Cross-references: UNIPROT:P24100; EMBL:D10850; NID:g217848; PID:BAA01623.1; PID:g2178
R;Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.
Biochem. Soc. Trans. 20, 80-84, 1992
A;Title: Control of cell division in plants.
A;Reference number: A48984; MUID:92339744; PMID:1634002
A;Accession: A48984
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-294 <INZ>
A;Experimental source: flower
A;Note: sequence extracted from NCBI backbone (NCBIP:109461)
R;Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.
Gene 105, 159-165, 1991
A;Title: Identification of two cell-cycle-controlling cdc2 gene homologs in Arabidopsis
A;Reference number: JQ1337; MUID:92039027; PMID:1937013
A;Accession: JQ1337
A;Molecule type: mRNA
A;Residues: 1-294 <HIF>
A;Cross-references: EMBL:X57839; NID:g16218; PID:CAA0971.1; PID:g16219
R;Ferreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze, D.
Plant Cell 3, 531-540, 1991
A;Title: The Arabidopsis functional homolog of the p34cdc2 protein kinase.
A;Reference number: JQ0967; MUID:93005715; PMID:1840925
A;Accession: JQ0967
A;Molecule type: mRNA
A;Residues: 1-294 <PER>
A;Cross-references: GB:S45387; NID:g257373; PIDN:AAB23643.1; PID:g257374
A;Experimental source: flower
C;Comment: The protein is a key component of the eukaryotic cell cycle.
C;Genetics:
A;Gene: cdc2
A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3
C;Function:
A;Description: phosphotransferase; protein kinase; required for G1 to S-phase transition
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.3%; Score 551.5; DB 2; Length 294;
Best Local Similarity 35.5%; Pred. No. 2.2e-18;
Matches 115; Conservative 71; Mismatches 95; Indels 43; Gaps 8;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFESDDPVVKKTALREIRMLKQLKH 60
Db 1 MDQYKEKIGEGTYGVVYKARDKVTNETIALKIRLEQDEGVFSTAIRISLLKEMQH 60
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Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVAD-GVIKSVLWOTLQALNECHI 119
Db 61 SNIVKLDQVHVHSEKRLYLVEYLDLQKGMDSPTDFSKOLHMIKTKLYLQIRGIAYCHS 120
Qy 120 HNCIHRDKPENILITKO-GIIKICDFGFAQIL-IPGDAYTVVATRYRAPELLVGDQ 177
Db 121 HRVLRDLKFNQLIDRRTNLSKLADFLARAGIPVRTTHEVTVLWYRAPELLASHH 180
Qy 178 YGSSVDIWAIGCVFAELLTQQLPMPGKSDVDQLYLIR---TLVETGFRHVDQAGLELL 234
Db 181 YSTPVDIWSVGCIFAEMISQKPLFPGBSEIDQLFKIFRIMGTPYEDTWR----- 229
Qy 235 SSDPPAVASQASGAGITCKLIPRHQSIFKSGFFHGISIPEDMETLEEKFSVDHPVALNF 294
Db 230 -----GVTS--LPDYKSAPFK-----WKPTDLETF--VPNLDPDGDVL 263
Qy 295 MKGCLMNPDDRLTCSQLLESSYF 318
Db 264 LSKMLMDPTKRINARAALAEHYF 287

RESULT 11
A40444
protein kinase (EC 2.7.1.37) cdc2 homolog A - maize
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A40444
R;Colasanti, J.; Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A;Title: Isolation and characterization of cDNA clones encoding a functional p34 (cdc2) hc
A;Reference number: A40444; MUID:91195354; PMID:2014258
A;Accession: A40444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-294 <COL>
A;Cross-references: GB:M60526
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.0%; Score 546.5; DB 1; Length 294;
Best Local Similarity 34.1%; Pred. No. 3.6e-18;
Matches 117; Conservative 66; Mismatches 93; Indels 67; Gaps 9;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFESDDPVVKKTALREIRMLKQLKH 60
Db 1 MEQYKEKIGEGTYGVVYKALDKTANETIALKIRLEQDEGVFSTAIRISLLKEMNH 60
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPNGVADGVKSVLWOTLQAL 114
Db 61 GNIVLRHDVVHSEKRIYLVEYLDLQKFMDSCEFAKNT-----LIKSYLQILHGV 115
Qy 115 NFCHIHNCIHRDKPENILITKO-GIIKICDFGFAQIL-IPGDAYTVVATRYRAPELL 172
Db 116 AYCHSHRVLHRLDKPNQLIDRRTNLSKLADFLARAGIPVRTTHEVTVLWYRAPELL 175
Qy 173 VGDYQYSSVDIWAIGCVFAELLTQQLPMPGKSDVDQLYLIRTLVETGFRHVDQAGLEL 232
Db 176 LGARQYSTPVDVMSVGCIFAEMVQKPLFPDSEIDSLFKIFRLG----- 221
Qy 233 LTSDPPAVASQASGAGITCKLIPRHQSIFKSGFFHGIS-IP-----EPEDMETLEE 282
Db 222 -----TPNEQS-----WPGVSCLPDFKTAFFRMQAQDLATV-- 252
Qy 283 KFSVDHPVALNFMKGCLMNPDDRLTCSQLLESSYFDSFQEAQ 325
Db 253 -VPNLDPAGLDLLSKMLRYEPSKRITARQALEHEYFKDLEWVQ 294

RESULT 12
```

T49271

CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A - Arabidopsis thaliana
N;Alternate names: protein T21J18.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C;Accession: T49271
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25021
A;Accession: T49271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <R1E>
A;Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.20
A;Experimental source: cultivar Columbia; BAC clone T21J18
C;Genetics:
A;Gene: ATSP-T21J18.20
A;Map position: 3
A;Introns: 3/3; 67/3; 105/3; 163/3; 218/2; 247/3; 265/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 30.0%; Score 546.5; DB 2; Length 294;
Best Local Similarity 35.2%; Pred. No. 3.6e-18;
Matches 114; Conservative 71; Mismatches 96; Indels 43; Gaps 8;

QY 1 MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MDQYKVEKIGEGTYGVVYGRHKTGTQGVAMKIRLESEEG-VPTAIRISLLKELR 60
QY 61 PNLVNLIEVFRKRKMHLYFEYCDHTLLNELERNPNQVAD-GVKSVLVMTQLQALNFC 119
DB 61 SNIVKYDDVHSEKRLVLYFEYLDLKKHMDSTPDFSKLHMKTLYQLRLGIAYCHS 120
QY 120 HNCIHRDIKPNILITKQ-GIIKICDFGFAQIL-IPGDAYTDVATRYRAPELLVGDQ 177
DB 121 HRVLRDLKPQNLIDRTNSLKLADFGLARAFGIPRVTFHEVTVLWYRAPELLGSHH 180
QY 178 YGSSVDIWAIGCVFABLLTGQPLWPKSDVDQLYLIIR---TLVETGFRHVDQAGLELLT 234
DB 181 YSTPVDIWSVGCIFAEMISQKPLFPQSGEIDQLFKIFRIMGTPYEDTWR----- 229
QY 235 SSDPPAVASQASAGITGKLI PRHQSIFKSNFGFFHGISIPEDMETLEKSDVHPVALNF 294
DB 230 -----GVTS--LPDYKAFPK-----WKPTDLETF---VNLDPDQGVLD 263
QY 295 MKGCLKNPDRRLTCSOLLESSYF 318
DB 264 LSKMLMDPTKRINARAALHEYF 287

RESULT 13

A29539
N;Alternate names: cdc2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
R;Lee, M.G.; Nurse, P.
Nature 327, 31-35, 1987
A;Title: Complementation used to clone a human homologue of the fission yeast cell cycle
A;Reference number: A29539; MUID:87201915; PMID:3553962
A;Accession: A29539
A;Molecule type: mRNA
A;Residues: 1-297 <LEE>
A;Cross-references: UNIPROT:P06493; GB:X05360; NID:g29838; PIDN:CAA29863.1; PID:g29839
C;Genetics:
A;Gene: GDB: CDC2
A;Cross-references: GDB:119052; OMIM:116940
A;Map position: 10q21.1-10q21.1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif

F;14,161/Binding site: phosphate (Thr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 29.9%; Score 545; DB 2; Length 297;
Best Local Similarity 40.2%; Pred. No. 4.2e-18;
Matches 117; Conservative 58; Mismatches 74; Indels 42; Gaps 7;

QY 1 MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFF-VESEDDPVVKKIALREIRMLKQLKH 59
DB 1 MEDVTKEKIGEGTYGVVYGRHKTGTQGVAMKIRLESEEG-VPTAIRISLLKELR 59
QY 60 HPNLVNLIEVFRKRKMHLYFEYCDHTLLNELERNPNQ--VADGVIVKSVLWMTQLQALNFC 117
DB 60 HPNIVSLQDVLMDQSRLLYLFELSLMDLKKYLDSPFGQYMDSSLVSKSYLYQLQGVVFC 119
QY 118 HNCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDVATRYRAPELLVGD 176
DB 120 HSRVLRDLKPQNLIDDKGTIKLADFGLARAFGIPRVTFHEVTVLWYRAPELLG 179
QY 177 QYSSVDIWAIGCVFABLLTGQPLWPKSDVDQLYLIIRTL----- 217
DB 180 RYSTPVDIWSIGTIFABELATKPLFHGDSRIDQLFRIFALGTNNNEVWPEVESLQDYKN 239
QY 218 -----VETGFRHVDQAGLELLTSS---DPPAVASQASAGITGKLI PRH 256
DB 240 TFPKWKPGSLASHVKNLNDLGLSLKQLIYDP-----AKRISGRKALNH 284

RESULT 14

A44878
protein kinase (EC 2.7.1.37) cdk2 [validated] - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A44878
R;Hirai, T.; Yamashita, M.; Yoshikuni, M.; Tokumoto, T.; Kajiuza, H.; Sakai, N.; Nagahama
Dev. Biol. 152, 113-120, 1992
A;Title: Isolation and characterization of goldfish cdk2, a cognate variant of the cell
A;Reference number: A44878; MUID:92331802; PMID:1339336
A;Accession: A44878
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <HIR>
A;Cross-references: UNIPROT:P43450; GB:S40289; NID:g251619; PIDN:AAB22550.1; PID:g251620
A;Experimental source: oocyte
A;Note: sequence extracted from NCBI backbone (NCBIN:108782, NCBI:P:108783)
C;Genetics:
A;Gene: cdk2
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-255/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 29.9%; Score 545; DB 1; Length 298;
Best Local Similarity 46.6%; Pred. No. 4.2e-18;
Matches 102; Conservative 48; Mismatches 67; Indels 2; Gaps 2;

QY 1 MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MESFQKVEKIGEGTYGVVYGRHKTGTQGVAMKIRLESEEG-VPTAIRISLLKELN 60
QY 61 PNLVNLIEVFRKRKMHLYFEYCDHTLLNELERNPNQVADGVIVKSVLWMTQLQALNFC 119
DB 61 PNLVNLHVDIHTENKLYLVFEFLHQLDKRFMDSSVTGSLPLVKSYLELLQGLAFCHS 120
QY 120 HNCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDVATRYRAPELLVGD 178
DB 121 HRVLRDLKPQNLIDDKGTIKLADFGLARAFGIPRVTFHEVTVLWYRAPELLGCKY 180
QY 179 GSSVDIWAIGCVFABLLTGQPLWPKSDVDQLYLIIRTL 217
DB 181 STAVDIWSLGCIFAEWITRKALFFQDSEIDQLFRIFRTL 219

```

RESULT 15
145977
cyclin-dependent kinase 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: I45977
R:Yang, L.; Farin, C.E.
Gene 141, 283-286, 1994
A:Title: Identification of cDNAs encoding bovine cyclin B and Cdk1/cdc2.
A:Reference number: I45977; MUID:94215918; PMID:8163203
A:Accession: I45977
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-297 <YAN>
A:Cross-references: UNIPROT:P48734; GB:L26547; NID:g433155; PIDN:AAA18894.1; PID:g498173
C:Genetics:
C:Superfamily: kinase-related transforming protein; protein kinase homology
F:2-256/Domain: protein kinase homology <KIN>

Query Match          29.8%; Score 542; DB 2; Length 297;
Best Local Similarity 40.2%; Pred. No. 5,7e-18;
Matches 117; Conservative 57; Mismatches 75; Indels 42; Gaps 7;

Qy 1 MEYKELAKTGEQYGVVFKCRNKTSGQVAVKKF-VESEDDPVVKKIALREIRMLKOLK 59
Db 1 MEDVTKEIKEGTYGVVYKGRHKTGQVAMKKIRLESEEG-VPSTAIRISLLKELR 59

Qy 60 HPNLVNLIEVFRKRMHLVFEYCDHTLLNELERNPG--VADGVIKSVLWQTLQALNFC 117
Db 60 HPNTVSLQDVLMDQSRLLYIFEFSLMDLKKYLSIPPGQFMDSSLVKSYLYQILQGIIVFC 119

Qy 118 HHNCIHRDIKPNILITKGIKICDFGPAQIL-IPGDAYTDVATRWYRAPPELLVGD 176
Db 120 HSRVLRDLKPQNLIDDKGTIKLADFGLARAFGIPRVYTHEVTVLWRSPEVLGSA 179

Qy 177 QYSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTL----- 217
Db 180 GYSTPVDIWSIGTIFAEALATKKPLFHGDSIEDQLFRIFRALGTPNNEVWPEVESLQDYKS 239

Qy 218 -----VETGRHVDOAGLEILLTSS---DPPAVASQSAGITCKLIPRH 256
Db 240 TFPKWKPGSLASHVKNLDENGLDLLSKMLIYDP-----AKRISGRMALNH 284

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Search completed: April 22, 2005, 06:51:39
Job time : 29.3051 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:29:40 ; Search time 91.2054 Seconds
(without alignments)
1948.255 Million cell updates/sec

Title: US-10-766-691-10
Perfect score: 1820
Sequence: 1 MEKYEKLAKTGESYGVFK.....RKARNEGRRRQOVLPLKS 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1183.5	65.0	350	Q6AXJ9	Q6axj9 brachydanio
2	1180	64.8	352	Q8CEQ0	Q8ceq0 mus musculu
3	1162.5	63.9	358	Q6QUA0	Q6qua0 homo sapien
4	1158	63.6	352	Q6QHE7	Q6qhe7 rattus norv
5	1157.5	63.6	358	1 KIAA HUMAN	Q00532 homo sapien
6	1099.5	55.5	367	Q7QBG7	Q7qbg7 anopheles g
7	1001.5	55.0	353	Q9U2H1	Q9u2h1 caenorhabdi
8	1001.5	55.0	392	Q9VMN3	Q9vmn3 drosophila
9	941.5	51.7	566	Q9TTK0	Q9ttk0 oryctolagus
10	932	51.2	385	Q675R9	Q675r9 oikopleura
11	915.5	50.3	493	Q92772	Q92772 homo sapien
12	904.5	49.7	564	Q9QYI2	Q9qyi2 mus musculu
13	904.5	49.7	568	Q9QUR0	Q9quro mus musculu
14	902	49.6	329	Q9QYI1	Q9qyi1 mus musculu
15	899	49.4	320	Q6GMD6	Q6gmd6 xenopus lae
16	893.5	49.1	651	Q6TXH3	Q6txh3 rattus norv
17	758.5	41.7	455	Q9PLI4	Q9pli4 homo sapien
18	758.5	41.7	592	Q9IIV4	Q9iiv4 homo sapien
19	755	41.5	657	Q9BMG2	Q9bmg2 trypanosoma
20	744	40.9	353	Q8K134	Q8k134 mus musculu
21	743.5	40.9	1106	Q9GRT9	Q9grt9 leishmania
22	741.5	40.7	457	Q9BK32	Q9bk32 mus musculu
23	738.5	40.6	585	Q9BL49	Q9bl49 mus musculu
24	737.5	40.5	457	Q9JM02	Q9jmo2 rattus norv
25	737.5	40.5	505	Q9JM01	Q9jmo1 rattus norv
26	733.5	40.3	595	Q8BLF2	Q8blf2 mus musculu
27	694.5	38.2	783	Q9BWT8	Q9bwt8 mus musculu
28	694.5	38.2	831	Q8IYC7	Q8iyc7 homo sapien
29	694.5	38.2	1030	1 STK9 HUMAN	Q76039 homo sapien
30	682	37.5	993	2 Q8WXQ5	Q8wxq5 homo sapien
31	676.5	37.2	578	2 Q8BVE0	Q8bve0 mus musculu

32	618	34.0	1104	2	Q9W6R6	Q9w6r6 fugu rubrip
33	565.5	31.1	294	2	Q9ZRI1	Q9zri1 triticum ae
34	565	31.0	305	1	CDK3 HUMAN	Q00526 homo sapien
35	564	31.0	297	2	Q66IH7	Q66ih7 xenopus tro
36	563	30.9	302	1	CDK2 CARAU	P51958 carassius a
37	561	30.8	297	1	CDK2_XENLA	P23417 xenopus lae
38	558.5	30.7	292	1	CDK2H_DICDI	P34117 dictyosteli
39	558.5	30.7	340	2	Q7QKF5	Q7qkf5 anopheles g
40	556.5	30.6	289	2	Q7RM49	Q7rm49 plasmodium
41	555	30.5	297	2	Q6IRQ7	Q6irq7 xenopus lae
42	555	30.5	302	2	Q7T3L7	Q7t3l7 brachydanio
43	554	30.4	298	1	CDK2 HUMAN	P24941 homo sapien
44	551.5	30.3	294	1	CC21_ORYSA	P29618 oryza sativ
45	551.5	30.3	294	1	CC2A_ARATH	P24100 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q6AXJ9	PRELIMINARY;	PRT;	350 AA.
AC	Q6AXJ9;			
DT	25-OCT-2004 (TrEMBLrel. 28, Created)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE	Zgc:101002 protein.			
GN	Name=zgc:101002;			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SFRain-Singapore local strain; TISSUE=Embryo;			
RC	PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Ra Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SFRain-Singapore local strain; TISSUE=Embryo;			
RC	Director MGC Project;			
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC079506; AAH79506.1; -			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011003; Kinase_like.			
DR	InterPro; IPR00719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	InterPro; IPR001245; Tyr_pkinase.			
DR	Pfam; PF00069; Pkinase; I.			

60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Oneda Y., Ishikawa T., Okada K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX ADACHI J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK016781; HAC25497.1; -
DR HSP; G00535; I44L.
DR MGD; MGI:1918341; Cdk11.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR01009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 350 AA; 40810 MW; 9B04440EE038BE1 CRC64;
Query Match 65.0%; Score 1183.5; DB 2; Length 350;
Best Local Similarity 63.4%; Pred. No. 1.9e-72;
Matches 220; Conservative 47; Mismatches 45; Indels 35; Gaps 3;
QY 1 MEKYEKLAKTCEGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALRIRMLKQLKH 60
DB 1 MEKYEKISKIGESGYGVVFKCRNKTSGQVAVKVFVESEDDPIIKKIALRIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMLHVFYCDHTLNLNERNPNVADGVKSVLWOTLQALNFCIH 120
DB 61 PNLVNLMEVFRKRKMLHVFYCDHTLNLNERNPNVADGVKSVLWOTLQALNFCIH 120
QY 121 NCIRHDKPENILITKQGIKICDFGAQILI-PGDAYTDVYATRYRAPELLVGDYQYG 179
DB 121 NCIRHDKPENILITKQGIKICDFGAQILI-PGDAYTDVYATRYRAPELLVGDYQYG 180
QY 180 SSVDIWAIGCVFAELITGQPLWPKSDVDOLVLIIRTLVETGFRHVDQAGLELITSSDPP 239
DB 181 PFVDVWAVGCVFAELLSGAPLWPKSDVDOLVLIIRKTL----- 218
QY 240 AVASQAGITGKLIPIHQSIKSNFGPHGISIPEPEMETLEEFSDVHPVPMFMKGCL 299
DB 219 -----GELIPHQQVFTNQFFSGVCVPEPEMELELKYPNLSYQALSLMGCL 268
QY 300 KMPDRLTCSOLLESSYDSFQE--AQIKRKARNEGRNRRRQVILP 344
DB 269 RMDPAERLSCQLLEQYFDSURESESVTRELDRKKTRQPRKHL 315
RESULT 2
Q8CEQO PRELIMINARY; PRT; 352 AA.
ID AC Q8CEQO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933411017 product:cyclin-dependent kinase-like 1
DE (CDC2-related kinase), full insert sequence.
GN Name=Cdk11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

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Db 121 NCIHRDVKPENILITKQSAIKLDFGFARLTGQDYDDVATRWTRSPPELLVGDQYQ 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 PPVDVWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 218
Qy 240 AVASQASAGITKGLIPRHSIFKSNFGFHGISIPEDMETLEEFKSDVHPVAFNFMKGCL 299
Db 219 -----GDLIPRHOQVFSNQYFSGVKIPDPEDMETLEEFKSDVHPVAFNFMKGCL 268
Qy 300 KMNPDRLTCSQLLESSYFDSFQSA-----OIKKARNENRRQ-----QVLP 344
Db 269 HMDPAERLTCEQLLHPYFDSIREVGLTROHDPARKTLRQSRKHLTGQLYLP 322

RESULT 3
Q6QUAO PRELIMINARY; PRT; 358 AA.
ID Q6QUAO
AC Q6QUAO;
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Cyclin-dependent kinase-like 1 (CDC2-related kinase).
GN Name=CDKL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY525548; AAS000095.1; --
DR HSP; P23941; 1838.
DR GO; GO:0005534; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Cyclin; Kinase; Transferase.
SQ SEQUENCE 358 AA; 41833 MW; 823E432BF84B77C6 CRC64;

Query Match 63.9%; Score 1162.5; DB 2; Length 358;
Best Local Similarity 63.8%; Pred. No. 5.2e-71;
Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;

Qy 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKPFVSEDDPVVKIKALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGESGVVFKCRNKTSGQVAVKPFVSEDDPVVKIKALREIRMLKQLKH 61
Qy 61 PNLVNLLEVERKRLHVPYCDHTLLNELRPNPGVADGVIVKSVLQTLQALNFCIH 120
Db 62 PNLVNLLEVERKRLHVPYCDHTLLNELRPNPGVADGVIVKSVLQTLQALNFCIH 121
Qy 121 NCIHRDVKPENILITKQSAIKLDFGFARLTGQDYDDVATRWTRSPPELLVGDQYQ 179
Db 122 NCIHRDVKPENILITKQSAIKLDFGFARLTGQDYDDVATRWTRSPPELLVGDQYQ 181

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Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDVWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 219
Qy 240 AVASQASAGITKGLIPRHSIFKSNFGFHGISIPEDMETLEEFKSDVHPVAFNFMKGCL 299
Db 220 -----GDLIPRHOQVFSNQYFSGVKIPDPEDMETLEEFKSDVHPVAFNFMKGCL 269
Qy 300 KMNPDRLTCSQLLESSYFDSFQSAIKRKAARNE 333
Db 270 HMDPTERLTCEQLLHPYFDSIREVGLTROHDPARKTLRQSRKHLTGQLYLP 303

RESULT 4
Q6GHE7 PRELIMINARY; PRT; 352 AA.
ID Q6GHE7
AC Q6GHE7;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toohyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081896; AAH81896.1; --
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR002719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 40899 MW; DB9CDF5464E66E24 CRC64;

Query Match 63.6%; Score 1158; DB 2; Length 352;
Best Local Similarity 62.6%; Pred. No. 1e-70;
Matches 214; Conservative 45; Mismatches 49; Indels 34; Gaps 3;

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QY 1 MEKYEKLAKTGEGSGVWFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 DB 1 MEKYEKIGKIGSGVWFKCRNRTGQVAKRFLETTEDDPVKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 DB 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 QY 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
 DB 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 180
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 DB 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVAFNFMKGL 299
 DB 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVAFNFMKGL 299
 QY 300 KMPDDRLTCSQLLESSYFDSFOEQ-AQIKRKARNEGRNRQ 340
 DB 300 KMPDDRLTCSQLLESSYFDSFOEQ-AQIKRKARNEGRNRQ 340
 QY 269 HMDPRLTCSQLLOHPYFDSIRVDGELARPHDKPRTKRLQ 310
 DB 269 HMDPRLTCSQLLOHPYFDSIRVDGELARPHDKPRTKRLQ 310

RESULT 5

QY 1 MEKYEKLAKTGEGSGVWFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 DB 1 MEKYEKIGKIGSGVWFKCRNRTGQVAKRFLETTEDDPVKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 DB 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 QY 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
 DB 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 180
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 DB 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVAFNFMKGL 299
 DB 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVAFNFMKGL 299
 QY 300 KMPDDRLTCSQLLESSYFDSFOEQ-AQIKRKARNEGRNRQ 340
 DB 300 KMPDDRLTCSQLLESSYFDSFOEQ-AQIKRKARNEGRNRQ 340
 QY 269 HMDPRLTCSQLLOHPYFDSIRVDGELARPHDKPRTKRLQ 310
 DB 269 HMDPRLTCSQLLOHPYFDSIRVDGELARPHDKPRTKRLQ 310

ProDom; PD000001; Prot_kinase; 1.
 SMART; SM00220; S_TKC; 1.
 PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 5 288 Protein kinase.
 FT NP_BIND 11 19 ATP (By similarity).
 FT BINDING 34 34 ATP (By similarity).
 FT ACT_SITE 127 127 Proton acceptor (By similarity).
 SQ SEQUENCE 358 AA; 41834 MW; 88344321P24B77C6 CRC64;

Query Match 63.6%; Score 1157.5; DB 1; Length 358;
 Best Local Similarity 64.7%; Pred. No. 1.1e-70;
 Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;

QY 1 MEKYEKLAKTGEGSGVWFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 DB 2 MEKYEKIGKIGSGVWFKCRNRTGQVAKRFLETTEDDPVKKIALREIRMLKOLKH 61
 QY 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 DB 62 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 121
 QY 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
 DB 122 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 181
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 DB 182 PVDVWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVAFNFMKGL 299
 DB 220 -----GDLPFHQQVFSNQYFSGVKIPDPEDMEFLKFPFNISYPALGLKGL 269
 QY 300 KMPDDRLTCSQLLESSYFDSFOEQ 325
 DB 270 HMDPRLTCSQLLOHPYFDSIRVDGELARPHDKPRTKRLQ 295

RESULT 6

QY 1 MEKYEKLAKTGEGSGVWFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 DB 1 MEKYEKIGKIGSGVWFKCRNRTGQVAKRFLETTEDDPVKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 DB 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCHIH 120
 QY 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 179
 DB 121 NCIIHRDIPENILITKQIIKICDFGFAQILI-PGDAYTDYVATRYRPAPELLVGDTOYG 180
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 DB 182 PVDVWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTVETGFRHVDQAGLELLTSSDPP 239
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVAFNFMKGL 299
 DB 220 -----GDLPFHQQVFSNQYFSGVKIPDPEDMEFLKFPFNISYPALGLKGL 269
 QY 300 KMPDDRLTCSQLLESSYFDSFOEQ 325
 DB 270 HMDPRLTCSQLLOHPYFDSIRVDGELARPHDKPRTKRLQ 295


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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN 1.
KW ATP-binding; Hypothetical protein; kinase; Transferase.
SQ SEQUENCE 353 AA; 40665 MW; 7E3226D9849CAC9 CRC64;

Query Match          55.0%; Score 1001.5; DB 2; Length 353;
Best Local Similarity 53.4%; Pred. No. 4.3e-60;
Matches 187; Conservative 59; Mismatches 63; Indels 41; Gaps 3

Qy 1 MEKYEKLAKTGEYSGYVFKCRNKTSGOVAVKKPFVESEDDPVVKIALREIRMLKQLKH 60
Db   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
    1 MDKYRLSKLGEYSGYVYCKNRDTCGIVAICKFVETEDDPHIKKIALREIRMLKQLKH .60

Qy 61 PNLVNLIEVFERRKRKMHLVFEYCDHTLLNELERPNGVADGVIVKSVLWQTLOALNFCHH 120
Db   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    61 QNLVGLIEVFERNRKLHLVFLCDDRTVYLHELEKNPHGVNDLIKKIYYQLLEALKFCFSH 120

Qy 121 NCTHRDIKPNILITKGIIKICDFGFAQILI PGDAYTDVVATRYAPPELLVGDTQVS 180
Db   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    121 KCLHDRVKPNIFLRDNQDKLFGFARIINTMTDYVATRYSPPELLVGDVQYGP 180

Qy 181 SVDIWAIGCVFAELLTGQPLMPGKSDVDQLYLIIRTLVETGFRRHVDAQGLELLTSSDPPA 240
Db   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    181 PVDIWAIGCVYAELLTGSAIMPGESIDQLYHIRKTL----- 217

Qy 241 VASQSAGITGKIIPRHOSIFPKSNGFFHGISIPEPEDMETLEEKFSVDHPVALNFMKGCLK 300
Db   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    218 -----GEFLPRHSISIFRTNQFFGLSIPEHLEPLPSKLPNASSAQDLFLQKCFE 268

Qy 301 MNPDRLTCSQLLESSYDFSQEAQIKRKARNEG-----RNRRQQOVLPL 345
Db   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
    269 MSPDRRPSCELMHGI FSNW---ILRIODESTPTGLTSKRSPNYLP 314
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RESULT 8
Q9VMN3 PRELIMINARY; PRT; 392 AA.
AC Q9VMN3
AC Q9VMN3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG7236-PA.
GN ORFNames-CG7236;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RS SEQUENCE FROM N.A.
RP RP
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatzides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bröttier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glödeke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;
Qy 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNVLNLEVFRRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCFHH 120
Db 61 ENVLNLEVFRRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCFHH 120
Qy 121 NCIRHDKPENILITKQGIKICDFGPAQIL-IPCDAYTDVATRWYRAPELLVGDQY 179
Db 121 NCIRHDKPENILITKQGIKICDFGPAQIL-IPCDAYTDVATRWYRAPELLVGDQY 180
Qy 180 SSVDIWAGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 180 SSVDIWAGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Qy 240 AVASQAGITGKLIIPRQSIKFNKNGFFHG--ISIPEDMETLEEFSDVHPVALNFMKGL 299
Db 240 AVASQAGITGKLIIPRQSIKFNKNGFFHG--ISIPEDMETLEEFSDVHPVALNFMKGL 299
Qy 269 HVPDPKRPFCALLHDDFFQMDGFAERFSQELQMKVQKQDARNISLSKSKQNRKKEK 324
Db 269 HVPDPKRPFCALLHDDFFQMDGFAERFSQELQMKVQKQDARNISLSKSKQNRKKEK 324
Qy 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGRNRRQO 341
Db 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGRNRRQO 341
Qy 675R9 PRELIMINARY; PRT; 385 AA.
Db 675R9 PRELIMINARY; PRT; 385 AA.
Qy 25-OCT-2004 (TrEMBLrel. 28, Created)
Db 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Qy 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Db 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Qy Cyclin-dependent kinase-like 1.
Db Cyclin-dependent kinase-like 1.
Qy ORNames=006-03;
Db ORNames=006-03;
Qy Oikopleura dioica.
Db Oikopleura dioica.
Qy Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
Db Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
Qy Oikopleuridae; Oikopleura.
Db Oikopleuridae; Oikopleura.
Qy NCBI_TaxID=34765;
Db NCBI_TaxID=34765;
Qy SEQUENCE FROM N.A.
Db SEQUENCE FROM N.A.
Qy PubMed=1534333; DOI=10.1038/nature02709;
Db PubMed=1534333; DOI=10.1038/nature02709;
Qy Hansen A., Flaet M., Weissenbach J., Lehrach H., Wincker P.,
Db Hansen A., Flaet M., Weissenbach J., Lehrach H., Wincker P.,
Qy Reinhardt R., Chourrout D.;
Db Reinhardt R., Chourrout D.;
Qy "Hox cluster disintegration with persistent anteroposterior order of
Db "Hox cluster disintegration with persistent anteroposterior order of
Qy expression in Oikopleura dioica."
Db expression in Oikopleura dioica."
Qy Nature 431:67-71(2004).
Db Nature 431:67-71(2004).
Qy EMBL; AY449462; AAS21447.1; -
Db EMBL; AY449462; AAS21447.1; -
Qy GO; GO:0016301; F:kinase activity; IBA.
Db GO; GO:0016301; F:kinase activity; IBA.
Qy InterPro; IPR011009; Kinase like.
Db InterPro; IPR011009; Kinase like.
Qy InterPro; IPR000719; Prot_kinase.
Db InterPro; IPR000719; Prot_kinase.
Qy InterPro; IPR002290; Ser_thr_kinase.
Db InterPro; IPR002290; Ser_thr_kinase.
Qy InterPro; IPR008271; Ser_thr_pkin_AS.
Db InterPro; IPR008271; Ser_thr_pkin_AS.
Qy InterPro; IPR001245; Tyr_kinase.
Db InterPro; IPR001245; Tyr_kinase.
Qy Pfam; PF00069; Pkinase; 1.
Db Pfam; PF00069; Pkinase; 1.
Qy ProDom; PD000001; Prot_kinase; 1.
Db ProDom; PD000001; Prot_kinase; 1.
Qy SMART; SM00220; S_TKC; 1.
Db SMART; SM00220; S_TKC; 1.
Qy SMART; SM00219; Tyr_KC; 1.
Db SMART; SM00219; Tyr_KC; 1.
Qy PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Db PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Qy PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
Db PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
Qy Cyclin; Kinase.
Db Cyclin; Kinase.
Qy SEQUENCE 385 AA; 45512 MW; 059F814421AGADAL CRC64;
Db SEQUENCE 385 AA; 45512 MW; 059F814421AGADAL CRC64;

Query Match 51.2%; Score 932; DB 2; Length 385;

Best Local Similarity 52.2%; Pred. No. 2.5e-55;

Matches 168; Conservative 58; Mismatches 62; Indels 34; Gaps 2;

Qy 2 EKYEKLAKTGEISGVVFKCRNKTSGQVAVKPFVESEDDPVVKKIALREIRMLKQLKH 61

Db 4 DYEKIEKISGEISGVVFKCRNKTSGQVAVKPFVESEDDPVVKKIALREIRMLKQLKH 63

Qy 62 NLNVLIEVFRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCFHH 121
Db 64 NLNVLIEVFRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCFHH 123
Qy 122 CIHRDIPENILITKQGIKICDFGPAQIL-IPCDAYTDVATRWYRAPELLVGDQY 181
Db 124 CIHRDIPENILITKQGIKICDFGPAQIL-IPCDAYTDVATRWYRAPELLVGDQY 183
Qy 182 VDIWAGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 241
Db 184 VDIWAGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 241
Qy 242 ASQAGITGKLIIPRQSIKFNKNGFFHG--ISIPEDMETLEEFSDVHPVALNFMKGL 299
Db 219 -----CGELITQHKLLQTNKYLGRHLLTSPRPRVPIEALYKAPSTITISFLKNCL 271
Qy 300 KMPDDRLTCSQLLESSYFDSF 321
Db 272 QMDTMRDLDCVELLDHAYFDY 293
Qy 92772 PRELIMINARY; PRT; 493 AA.
Db 92772 PRELIMINARY; PRT; 493 AA.
Qy 01-FEB-1997 (TrEMBLrel. 02, Created)
Db 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Qy 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Db 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Qy P56 KXIAME protein kinase.
Db P56 KXIAME protein kinase.
Qy Name=KXIAME;
Db Name=KXIAME;
Qy Homo sapiens (Human).
Db Homo sapiens (Human).
Qy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Qy NCBI_TaxID=9606;
Db NCBI_TaxID=9606;
Qy SEQUENCE FROM N.A.
Db SEQUENCE FROM N.A.
Qy MEDLINE=97152547; PubMed=9000130;
Db MEDLINE=97152547; PubMed=9000130;
Qy Taglienti C.A., Wysek M., Davis R.J.;
Db Taglienti C.A., Wysek M., Davis R.J.;
Qy "Molecular cloning of the epidermal growth factor-stimulated protein
Db "Molecular cloning of the epidermal growth factor-stimulated protein
Qy kinase p56 KXIAME."
Db kinase p56 KXIAME."
Qy Oncogene 13:2563-2574(1996).
Db Oncogene 13:2563-2574(1996).
Qy -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
Db -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
Qy EMBL; U35146; AAC50918.1; -
Db EMBL; U35146; AAC50918.1; -
Qy HSP; P24941; LH00.
Db HSP; P24941; LH00.
Qy Genew; HGNC:1782; CDKL2.
Db Genew; HGNC:1782; CDKL2.
Qy GO; GO:0004672; P:protein kinase activity; TAS.
Db GO; GO:0004672; P:protein kinase activity; TAS.
Qy GO; GO:0007548; P:sex differentiation; TAS.
Db GO; GO:0007548; P:sex differentiation; TAS.
Qy GO; GO:0007165; P:signal transduction; TAS.
Db GO; GO:0007165; P:signal transduction; TAS.
Qy Pfam; PF00069; Pkinase; 1.
Db Pfam; PF00069; Pkinase; 1.
Qy ProDom; PD000001; Prot_kinase; 1.
Db ProDom; PD000001; Prot_kinase; 1.
Qy SMART; SM00220; S_TKC; 1.
Db SMART; SM00220; S_TKC; 1.
Qy PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
Db PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
Qy PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Db PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Qy PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Db PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Qy ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
Db ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
Qy SW SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;
Db SW SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;

Query Match 50.3%; Score 915.5; DB 2; Length 493;

Best Local Similarity 48.3%; Pred. No. 4.3e-54;

Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60

Db 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNVLNLEVFRRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCFHH 120

Db 61 ENVLNLEVFRRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCFHH 120

Qy 121 NCIRHDKPENILITKQGIKICDFGPAQIL-IPCDAYTDVATRWYRAPELLVGDQY 179

Db 121 NCIRHDKPENILITKQGIKICDFGPAQIL-IPCDAYTDVATRWYRAPELLVGDQY 180

QY	180	SSVDIWAIGCVFAELLTGQPIWPGKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP	233
Db	181	KAVDIWAIGCLVTEMFGMSFLPGSDIDQLIHMMCL	218
QY	240	AVASQASGITGKLIIPRHQSIFKSNFGFFHGISIPEDMETLEKEFSDVHPVALNFMKGL	299
Db	219	-----GNLIIPRHQELFNKNPVFAGVRUPEIKEREPLERRYPKSEVVVIDLAKKCL	268
QY	300	KNPNPDRITCSOLLESSVF--DSF-----QEAQIK--RKARN-----EGNRERRQ	341
Db	269	HIDPDKRPFCAELLHHDFQMDGFAERFSQELQLKVQKDARNVLSKKSKQNKKEK	324
RESULT 12			
Q9QY12	10	PRELIMINARY; PRT; 564 AA.	
AC	Q9QY12;		
DT	01-MAY-2000 (TREMELrel. 13, Created)		
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)		
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)		
DE	Ser/Thr kinase KKIARE-gamma.		
GN	Name=Cdk12; Synonyms=Kkm;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID=10090;			
FN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RA	Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
CC	-I- SMILARITY: Belongs to the Ser/Thr protein kinase family.		
CC	EMBL; AB029066; BAA8428.1; --		
DR	HSSP; P24941.1OIQ.		
DR	MGD; MGI-1856227; Cdk12		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR011009; Kinase like.		
DR	InterPro; IPR00719; Prot. kinase.		
DR	InterPro; IPR002290; Ser_Thr_pkinase.		
DR	InterPro; IPR008271; Ser_Thr_pkin_AS.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	ProDom; PD000001; Prot. kinase; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.		
DR	PROSITE; PS00113; PROTEIN KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SQ	SEQUENCE 564 AA; 63640 MW; DACDF630CCE82D5 CRC64;		
Query Match			
Best Local Similarity 49.7%; Score 904.5; DB 2; Length 564;			
Matches 174; Conservative 66; Mismatches 69; Indels 49; Gaps 7;			
QY	1	MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFEVSEDDPVVKYIALREIMLKOLKH	60
Db	1	MEKENLGLVGECSYGVGMVKCRNKDSGRIVAIAKFFLESDDDKMVKYIAMREIKLKQLRH	60
QY	61	PNLVNLTIEVRRKRKMLVFECYCDHTLLNELRNPNGVADGVIKSVLWQTLQALNFCIH	120
Db	61	ENLVNLTVECKKKRWLVFEFVDHTILDDLKLFNGLDVQVQKYLFOINGIGFCHSH	120
QY	121	NCHIRDIKPNILITKQGIKICDFGPAQL-IPGDAYTDVATRWYRAPPELLVGDQYQ	179
Db	121	NI1HRIKPNILVSGSVKLCDFGPAFLAAGPEVYTDVATRWYRAPPELLVGDVKYQ	180
QY	180	SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP	239
Db	181	KAVDIWAIGCLVTEMFGMSFLPGSDIDQLIHMMCL	218
QY	240	AVASQASGITGKLIIPRHQSIFKSNFGFFHGISIPEDMET--LEEKFSDVHPVALNFMKG	297

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Qy 240 AVASQSAGITCKLIPRHOSIFKSNKFFHGISIPEDMET--LEEKSDVHPVALNFMKG 297
Db 219 -----GNLIPRHQELFYKPVFAGVRLPEVKDAEAPLESRYPKUPEAVISLAKK 268
Qy 298 CLKWNPDRLTCSOLLESSYF--DSF-----QEAQIK--RKARN-----EGNRRRROQ 341
Db 269 CLHIDPDKRPFCAULLRHDFQMDGFAERFSQELQLKIEKDARNNSLPKKSQNRKKEK 326

RESULT 14
ID Q9QY11 PRELIMINARY; PRT; 329 AA.
AC Q9QY11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ser/Thr kinase KIAMRE-delta (Fragment).
GN Name=Cdk12; Synonyms=Kkm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB029067; BA088429.1; --
DR HSSP; P24941; 10IQ
DR MGD; MGI:1858227; Cdk12.
DR GO; GO:0005534; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:proteinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 329 329
FT SEQUENCE 329 AA; 38023 MW; F72EB89E65AE8595 CRC64;

Query Match 49.6%; Score 902; DB 2; Length 329;
Best Local Similarity 49.0%; Pred. No. 2.3e-53;
Matches 173; Conservative 63; Mismatches 73; Indels 44; Gaps 6;

Qy 1 MEKYEKLAKTCEGSGYGVFKCRNTKSGQVAVKFESEDDPVVKYKALREIMLKQKH 60
Db 1 MEKYEGLVGEISGYGMVKMKDSCRVAIKFLESDDDKMKVKIAMREIKLLQRLH 60
Qy 61 PNLVNLIEVFRKRMHLVPEYCDHTLLNELRPNPGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLIEVCKKRWLVPEFVDHTILDLLKLPNGLDYGVQVKYLFQINGIGFCHSH 120
Qy 121 NCIHRIKPNILITKQGIKICDPGFAQIL-IPGDAYTVYATRWYRAPELLVGDYQYG 179
Db 121 NIHRIKPNILVSQSGVVKLCDFGARTLAAPGVVTVYATRWYRAPELLVGDYQYG 180
Qy 180 SSVDIWAIGCVFALLTGQPLWPKGSVDQYLYLIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDIWAIGCVLIVEMLQGLPFGESIDQLHMTCL----- 218
Qy 240 AVASQSAGITCKLIPRHOSIFKSNKFFHGISIPEDMET--LEEKSDVHPVALNFMKG 297
Db 219 -----GNLIPRHQELFYKPVFAGVRLPEVKDAEAPLESRYPKUPEAVISLAKK 268
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Qy 298 CLKWNPDRLTCSOLLESSYF--DSF-----QEAQIK--RKARNEGNNRRROQ 341
Db 269 CLHIDPDKRPFCAULLRHDFQMDGFAERFSQELQLKIEKDARNNSLPKKSQK 321

RESULT 15
ID Q6GMD6 PRELIMINARY; PRT; 320 AA.
AC Q6GMD6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC443693 protein (Fragment).
GN Name=LOC443693;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Browstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC074132; AAH74132.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 320 320
SQ SEQUENCE 320 AA; 37063 MW; 4CD2189603F9115F CRC64;

Query Match 49.4%; Score 899; DB 2; Length 320;
Best Local Similarity 48.8%; Pred. No. 3.5e-53;
Matches 169; Conservative 64; Mismatches 75; Indels 38; Gaps 4;

QY 1 MEKYKLAKTGSGYGVVFKCNKTSQGVAVKFESEDDPVVKKIALREIRMLKQLKH 60
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
1 MEKYENLGIVGSGYGMVKCRNKETGRIVAIIKKPLESEDDKMKVKIAMREIKLLQLRH 60
QY 61 PNLVNLIEVFRKKRMHLLVEFYCDHTLNELEENENGADVGVKSVLWQTLQALNFCHIH 120
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
61 ENLVNLEVCCKKKRWYLVFEFVDRTVLDDLEQFPNGLDENRVKYLFOIIRGIGFCHNH 120
QY 121 NCIIHRDIKPENILITKQGIHKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
121 NIIHRDIKPENILVLSGIVKLCDFGFARTLAGPGEDYTDYVATRWYRAPELLVGDIXYG 180
QY 180 SSVDIWAIGCVFAELLTCQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELITSSDPP 239
Db :||: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
181 KAVDVWAIGCVITVEMLTAAQLPFGSDSIDQLHHIK----- 216
QY 240 AVASQAGITKGLIPRHOSIFKSNGFHGISIPEDMETLEEKFSVDHPVALNFMKGCL 299
Db ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
217 -----CQGNLTPRHQELFYRPMFAGVSLPDKGAESLERRYPKHSPVMDLAKSCL 268
QY 300 KKNPDRLTCSQLLESSYF--DSFQE---AQIKRKARNEGNNRRRQ 340
Db :||: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
269 HIDPEKRPACGTLQLHELFTKDNFSERFSPQIRAKLQNLKDNSSQ 314

Search completed: April 22, 2005, 06:50:39
Job time : 98.2054 secs